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OM protein - protein search, using sw model

Run on: September 15, 2005, 15:50:48 ; Search time 121 Seconds
(without alignments)
41.553 Million cell updates/sec

Title: US-09-576-724-2

Perfect score: 72

Sequence: 1 CITQYQRESQAYY 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 716780

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	13	5	Abb08379 Immunogen
2	72	100.0	13	7	Add24247 Bovine pr
3	72	100.0	13	7	Adf65802 Prion pro
4	72	100.0	15	2	Aar38048 Prion pro
5	72	100.0	17	4	Aab69083 Bovine pr
6	72	100.0	19	5	Abb81632 Prion mim
7	72	100.0	19	8	Abu64310 Transmiss
8	72	100.0	19	8	Ado04597 Prion mim
9	69	95.8	13	5	Abb08378 Mutant in
10	69	95.8	13	7	Add24246
11	69	95.8	15	7	Adcs3154 Immunolog
12	69	95.8	18	5	Abb80955 Prion E3
13	68	94.4	20	7	Add24243 Mouse pr
14	63	87.5	12	8	Adl15228 Bovine pr
15	63	87.5	12	8	Adl15244 Bovine pr
16	59	81.9	11	8	Adl15241 Bovine pr
17	59	81.9	14	8	Adl15249 Bovine pr
18	59	81.9	15	8	Adl15264 Bovine pr
19	49	68.1	19	8	Adl15217 Bovine pr
20	40	55.6	12	6	Abp55131 Bovine pr
21	37	51.4	11	3	Aab15060 Human pri
22	37	51.4	12	2	Aaw35546 Immunizat
23	37	51.4	12	3	Aab15065 Sheep pri
24	37	51.4	12	3	Aab15064 Cattle pr
25	37	51.4	12	4	Aau25361 Schizophr

26	37	51.4	12	4	Aau15705
27	37	51.4	12	6	Abp55138 Human pri
28	37	51.4	12	8	Adl15218 Bovine pr
29	37	51.4	12	8	Adl15236 Bovine pr
30	37	51.4	12	8	Ado78972 Schizophr
31	37	51.4	15	8	Adl15261 Bovine pr
32	34	47.2	12	3	Aab15063 Mouse pri
33	34	47.2	12	3	Aab15062 Hamster p
34	34	47.2	16	2	Aaw54046 C. parvum
35	34	47.2	20	4	Aab66615 Mouse pri
36	32	44.4	8	6	Abp55135 Prion pro
37	32	44.4	17	2	Aay18295 Tendamist
38	32	44.4	20	8	Adh15361 Gliadin r
39	32	44.4	20	8	Adh16090 Gliadin r
40	32	44.4	20	8	Adh16091 Gliadin r
41	32	44.4	20	8	Adh15360 Gliadin r
42	31	43.1	6	4	Aab69081 Ovine con
43	31	43.1	13	5	Aae23853 Human zsi
44	31	43.1	13	5	Aae15898 Human zsi
45	31	43.1	14	8	Ado25670 S_pneumon

ALIGNMENTS

RESULT 1

ABB08379
ID ABB08379 standard; peptide; 13 AA.

XX AC

XX ABB08379;

DT 22-APR-2002 (first entry)

XX DE Immunogenic peptide derived from bovine prion protein.

XX KW Prion; BSE; bovine spongiform encephalopathy; vCJD;

KW new variant creutzfeldt jacobs disease; scrapie; TSE;

KW transmissible spongiform encephalopathy; antibody; PrPSc; PrPC; vaccine;

KW CJD; creutzfeldt jacobs disease; cow.

XX OS Bos taurus.

XX PN EP1158003-AL.

XX PD 28-NOV-2001.

XX PF 23-MAY-2000; 2000EP-00111108.

XX XX 23-MAY-2000; 2000EP-00111108.

XX (BLOO-) BLOOD TRANSFUSION CENT SLOVENIA.

XX PI Curin-Serbec;

XX WPI; 2002-107827/15.

PT New antibody, useful in diagnosis and treatment of BSE, CJD, new variant CJD and other Transmissible Spongiform Encephalopathy related diseases, selectively binds to the infectious form of the prion protein.

XX PS Claim 18; Page 11; 21pp; English.

CC The invention relates to an antibody selectively binding to the three dimensional conformation of the C-terminal of the infectious 'scrapie' (PrPSc) isoform of the prion protein (or a part), but not binding to the structure of the C-terminal of the normal cellular (PrPc) isoform of the prion protein. The antibodies (or functional parts) are useful in the diagnosis of Bovine Spongiform Encephalopathy (BSE), Creutzfeldt Jacobs Disease (CJD), new variant form CJD (vCJD) and other Transmissible Spongiform Encephalopathy (TSE) related diseases e.g. in humans, cows, sheep etc., since they can differentiate between the infectious (PrPSc) isoform and the normal cellular (PrPc) isoform of the prion protein. They are also useful in the treatment of such diseases. They may be included in

CC pharmaceutical compositions or used to produce drugs or active and/or
 CC passive vaccines against diseases as above. The anti-idiotypic antibodies
 CC of the polypeptides of the invention may also be used to produce drugs or
 CC vaccines against such diseases. The current sequence represents an
 CC immunogenic peptide derived from bovine prion protein C-terminal region
 CC (see AB08377)

SQ Sequence 13 AA;
 Query Match 100.0%; Score 72; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.6e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYQRESQAYY 13
 |||||
 Db 1 CITQYQRESQAYY 13

RESULT 2
 ADD24247
 ID ADD24247 standard; peptide; 13 AA.

AC ADD24247;

DT 15-JAN-2004 (first entry)

DE Bovine prion protein PrP peptide 225-237.

KW vaccine composition; virus-like particle; core particle;
 KW first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jakob Disease; prion.

OS prion.

XX W02003059386-A2.

XX 24-JUL-2003.

XX 17-JAN-2003; 2003WO-EP000460.

XX 18-JAN-2002; 2002US-00050902.

XX 21-JAN-2002; 2002WO-18000166.

XX 08-JUL-2002; 2002US-0393725P.

XX 18-JUL-2002; 2002US-0396590P.

XX (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX Bachmann M, Maurer P, Fellicoli E, Renner WA;

XX WPI; 2003-598483/56.

XX A vaccine composition for preventing or treating prion diseases (e.g.
 XX Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-
 XX phage) and at least one prion protein or peptide bound to the virus-like
 XX particle.

XX Disclosure; Page 86; 246pp; English.

XX This invention relates to a novel vaccine composition comprising a virus-
 XX like or a core particle with at least one first attachment site and at
 XX least one antigen or antigenic determinant that is a prion protein (PrP)
 XX or its dimer, or a PrP peptide, the antigen or antigenic determinant
 XX being bound to the virus-like or core particle. The vaccine of the
 XX invention may have neuroprotective or antiinflammatory activity. The
 XX composition is useful as a medicament or in manufacturing a medicament
 XX for the treatment or prevention of prion diseases. The prion diseases may
 XX include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
 XX Disease. The present sequence is that of a peptide fragment of a prion
 XX protein which may be used for the production of the vaccine of the
 XX invention.

SQ Sequence 13 AA;

Query Match 100.0%; Score 72; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.6e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYQRESQAYY 13
 |||||
 Db 1 CITQYQRESQAYY 13

RESULT 3
 ADF65802
 ID ADF65802 standard; protein; 13 AA.

XX ADF65802;

DT 12-FEB-2004 (first entry)

DE Prion protein derived immunogenic peptide #3.

KW chicken; antibody; prion protein;
 KW transmissible spongiform encephalopathy; epitope mapping;
 KW bovine spongiform encephalopathy; immunogenic; TSE; BSE.

XX Unidentified.

XX DE10219298-A1.

XX 06-NOV-2003.

XX 25-APR-2002; 2002DE-01019298.

XX 25-APR-2002; 2002DE-01019298.

XX (UYBE) UNIV BERLIN HUMBOLDT.

XX (VETE-) INST VETERINAER PHARMAKOLOGIE & TOXIKOLO.

XX Luskay K, Doberschuetz K, Henklein P, Schade R, Fischer L;

XX Sasse M;

XX WPI; 2003-866999/81.

XX New chicken antibodies against prion proteins, useful for diagnosis of
 XX transmissible, specifically bovine, spongiform encephalopathy.

XX Claim 6; Page 2; 6pp; German.

XX This invention describes novel chicken antibodies directed against
 XX mammalian prion proteins (Pr). The invention discloses a method for the
 XX production of such antibodies and a test system for diagnosis of
 XX transmissible spongiform encephalopathy comprising a homogenisation
 XX buffer, decomposition reagent, chicken antibodies, enzyme-labelled
 XX secondary antibody, colour and stop reagents, and sample buffer. Prion-
 XX specific sequences Asp-Arg-Tyr-Tyr-Arg-Glu-Asn-Met-His-Arg or Tyr-Tyr-Arg
 XX -Asp-Val-Asp-Gln-Tyr-Ser-Asn were detected by epitope mapping and used to
 XX generate the chicken antibodies by linking them to a high molecular
 XX weight carrier, e.g. keyhole limpet haemocyanin or bovine serum albumin
 XX and purifying the resulting antibodies by affinity chromatography. The
 XX products of the invention are used for diagnosis of transmissible
 XX spongiform encephalopathy (TSE), specifically bovine spongiform
 XX encephalopathy (BSE). This sequence represents a prion protein derived
 XX immunogenic peptide used to raise the antibodies described in the
 XX invention.

SQ Sequence 13 AA;

Query Match 100.0%; Score 72; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.6e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYQRESQAYY 13
 |||||

Db 1 CITQYQRESQAYY 13

RESULT 4

AA38048

ID AAR38048 standard; protein; 15 AA.

XX

AC AAR38048;

XX

DT 25-MAR-2003 (revised)

DT 14-OCT-1993 (first entry)

XX

DE Prion protein region F #2.

XX

KW Antigen; prion; protein; region; frame shift; repeat; mutation; PrPc;

KW F5a; F5b; subfragment; antibody; treatment; spongiform encephalopathy;

KW human; sheep; cattle; cellular binding; aggregation; mammal; scrapie;

KW immune system; PrPsc; ratio-inverso peptide; enzymatic degradation;

KW resistance.

XX

OS Synthetic.

XX

PN W09311155-A1.

XX

PD 10-JUN-1993.

XX

PF 03-DEC-1992; 92WO-GB002246.

XX

PR 03-DEC-1991; 91GB-00025747.

PR 10-JUL-1992; 92GB-00014663.

XX

PA (PROT-) PROTEUS MOLECULAR DESIGN LTD.

XX

PI Fishleigh RV, Robson B, Mee RP;

XX

DR WPI; 1993-196994/24.

XX

XX New polypeptide(s) contg. antigenic site of prion. protein - useful for

PT treatment and diagnosis of mammalian encephalopathies e.g. Creutzfeldt-

PT Jakob disease and kuru.

PT

XX

PS Claim 29; Page 74; 82pp; English.

XX

XX The sequences given in AAR38041-48 represent polypeptides which are

CC derived from an antigenic site, region F, of a prion protein. Prion

CC proteins comprise six regions of interest (A-F), and two related frame

CC shift peptides sequences caused by a repeating section in region E having

CC a nucleic acid coding sequence frame shift mutation of +1 (F5a) or -1

CC (F5b). These peptides (see also AAR38041-48) and antibodies raised

CC against these may be used to treat or prevent spongiform encephalopathy

CC in humans, sheep or cattle. They can be used to block cellular binding

CC and aggregation of prion proteins and to stimulate the mammalian immune

CC system. These peptides may be used to distinguish between the normal form

CC of prion protein (PrPc) and the scrapie-associated form (PrPsc). These

CC peptides may include rare or synthetic amino acids or a ratio- inverso

CC peptide modification to improve resistance to enzymatic degradation.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 72; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 4.2e-06;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYQRESQAYY 13

Db 1 CITQYQRESQAYY 13

RESULT 5

AA369083

ID AAB69083 standard; peptide; 17 AA.

XX

AC AAB69083;

XX

DT 23-APR-2001 (first entry)

XX

DE Bovine prion protein peptide SEQ ID NO:3.

XX

KW Monoclonal antibody; detection; prion protein; TSE; infection;

KW transmissible spongiform encephalopathy; scrapie; bovine encephalopathy;

KW chronic wasting disease; PrP-Sc.

XX

OS Bos taurus.

XX

PN W0200105426-A1.

XX

PD 25-JAN-2001.

XX

PF 14-JUL-2000; 2000WO-US019211.

XX

PR 15-JUL-1999; 99US-00353348.

XX

PA (USDA) US DEPT OF AGRICULTURE.

XX

PI O'rouke KI;

XX

DR WPI; 2001-159477/16.

XX

PT Monoclonal antibodies for detecting prior proteins as an indication of

PT transmissible spongiform encephalopathies, specifically binds to

PT conserved group of prior proteins.

XX

PS Example 2; Page 12; 25pp; English.

XX

XX The present invention describes a monoclonal antibody (I) which

CC specifically binds to a conserved epitope of prion proteins, which is

CC capable of binding prion protein (PrP)-Sc protein in fixed or unfixed

CC tissue that has been treated to unmask the group to PrP-Sc protein and

CC eliminate availability of a corresponding group of PrP-Cellular. (I) can

CC be used in immunoassays to detect PrP-Sc proteins in animal or human,

CC including ruminant livestock, cats, mink and non-human primates, sheep,

CC goat, cattle, mule deer and elk, as an indication of the presence of

CC transmissible spongiform encephalopathies (TSE). Presence of PrP-Sc

CC indicates the scrapie-, bovine encephalopathy- or chronic wasting disease

CC -infected animals. The antibodies provide early detection of PrP-Sc and

CC for preclinical diagnosis of TSE. The present sequence represents a prion

CC protein peptide which is used in an example from the present invention

XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 72; DB 4; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.8e-06;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYQRESQAYY 13

Db 1 CITQYQRESQAYY 13

RESULT 6

ABB81632

ID ABB81632 standard; peptide; 19 AA.

XX

AC ABB81632;

XX

DT 25-SEP-2002 (first entry)

XX

DE Prion mimetic peptide SEQ ID NO:4.

XX

KW Prion mimetic peptide; degradation; detection; TSE; infection;

KW transmissible spongiform encephalopathy; prion protein; sterilisation;

KW immunisation; Creutzfeldt-Jacob disease; kuru; fatal familial insomnia;

KW Gerstmann-Strausler-Scheinker syndrome; chronic wasting disease;

KW bovine spongiform encephalopathy; feline spongiform encephalopathy;

KW scrapie; transmissible mink encephalopathy.

XX OS Synthetic.
 XX PN WO200253723-A2.
 XX PD 11-JUL-2002.
 XX XX
 XX PF 08-JAN-2002; 2002WO-GB0000052.
 XX XX
 XX PR 08-JAN-2001; 2001GB-00000420.
 XX PR 26-FEB-2001; 2001GB-00004696.
 XX XX
 XX PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.
 XX XX
 XX PI Raven NDH;
 XX XX
 XX DR WPI; 2002-557743/59.
 XX XX
 XX PT Inactivating transmissible spongiform encephalopathy (TSE) agent such as
 XX PT Creutzfeldt-Jacob disease, scrapie, kuru or Gerstmann-Strausler-
 XX PT Scheinker syndrome involves exposing agent to thermostable proteolytic
 XX PT enzyme.
 XX PS Example; Page 19; 41pp; English.
 XX XX
 XX CC The present invention describes a method (M1) for inactivating a
 XX CC transmissible spongiform encephalopathy (TSE) agent comprising exposing
 XX CC the TSE agent to a thermostable proteolytic enzyme. Also described: (1) a
 XX CC composition (I) for inactivating a TSE agent, comprising a thermostable
 XX CC proteolytic enzyme; (2) an antibody (II) specific for a prion dimer which
 XX CC does not bind to a prion monomer; and (3) a purified prion dimer. (M1) is
 XX CC useful for inactivating a TSE agent such as a prion. A TSE agent is
 XX CC Creutzfeldt-Jacob disease or its variant, kuru, fatal familial insomnia,
 XX CC Gerstmann-Strausler-Scheinker syndrome, bovine spongiform
 XX CC encephalopathy, scrapie, feline spongiform encephalopathy, chronic
 XX CC wasting disease or transmissible mink encephalopathy. (I) is useful for
 XX CC sterilising material contaminated with the TSE agent. A prion dimer is
 XX CC useful for examining a sample infected with or suspected to be infected
 XX CC by a prion protein, and for detecting prion infectivity, by detecting a
 XX CC prion dimer in the sample. A prion dimer is useful for producing (II), by
 XX CC immunising an animal with a prion dimer, obtaining its extract which
 XX CC contains (II), and isolating (II) from the extract. The method comprises
 XX CC obtaining an antibody preparation containing antibodies which bind a
 XX CC prion dimer, and removing (II) from the preparation. (M1) and (I) are
 XX CC useful for inactivating TSE agents in potentially contaminated clinical
 XX CC waste and culled animal material. (M1) is useful for sterilising larger
 XX CC surface areas of apparatus, operating tables or even walls of rooms. The
 XX CC present sequence represents a prion mimetic peptide which is used in an
 XX CC example from the present invention in the preparation of antibodies
 XX CC including dimer preferential antibodies
 XX XX
 XX SQ Sequence 19 AA;
 Query Match 100.0%; Score 72; DB 5; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5.4e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CITQYQRESQAYY 13
 Db |||||
 1 CITQYQRESQAYY 13
 RESULT 7
 ABU64310
 ID ABU64310 standard; peptide; 19 AA.
 XX AC
 XX AC ABU64310;
 XX XX
 XX DT 11-MAR-2004 (first entry)
 XX XX
 XX DE Transmissible spongiform encephalopathy prion protein fragment #8.
 XX XX
 XX KW Transmissible spongiform encephalopathy; TSE; antibody; dimer;

KW antiinflammatory; neuroprotective; sedative.
 XX Unidentified.
 XX OS
 XX PN WO2003080665-A2.
 XX XX
 XX PD 02-OCT-2003.
 XX XX
 XX PF 20-MAR-2003; 2003WO-GB001295.
 XX XX
 XX PR 20-MAR-2002; 2002GB-00006584.
 XX PR 11-JUL-2002; 2002GB-00016098.
 XX XX
 XX PA (MICK-) MICROBIOLOGICAL RES AUTHORITY.
 XX XX
 XX PI Raven NDH, Sutton JM, Murdoch H;
 XX XX
 XX DR WPI; 2003-779246/73.
 XX XX
 XX PT Treating transmissible spongiform encephalopathy (TSE) infection
 XX PT comprises administering an antibody that binds to a dimer of a prion
 XX PT protein.
 XX PS Claim 5; Page 40; 40pp; English.
 XX XX
 XX CC The present invention relates to a method of treating transmissible
 XX CC spongiform encephalopathy (TSE) infection, comprising administering an
 XX CC antibody that binds to a dimer of a prion protein. The methods and
 XX CC compositions are useful for treating TSE, Creutzfeld-Jacob disease,
 XX CC variant Creutzfeld-Jacob disease, Kuru, fatal familial insomnia,
 XX CC Gerstmann-Strausler-Scheinker syndrome, bovine spongiform
 XX CC encephalopathy, scrapie, feline spongiform encephalopathy, chronic
 XX CC wasting disease and transmissible mink encephalopathy. Antigens are
 XX CC useful for the manufacture of a medicament for stimulating antibody
 XX CC production. The present sequence is a peptide fragment of a TSE prion
 XX CC protein
 XX SQ Sequence 19 AA;
 Query Match 100.0%; Score 72; DB 7; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5.4e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CITQYQRESQAYY 13
 Db |||||
 1 CITQYQRESQAYY 13
 RESULT 8
 ADO04597
 ID ADO04597 standard; peptide; 19 AA.
 XX AC
 XX AC ADO04597;
 XX XX
 XX DT 29-JUL-2004 (first entry)
 XX XX
 XX DE Prion mimetic peptide, 6.
 XX XX
 XX KW Transmissible spongiform encephalopathy; TSE; Creutzfeld-Jacob disease;
 XX KW Kuru; fatal familial insomnia; Gerstmann-Strausler-Scheinker syndrome;
 XX KW bovine spongiform encephalopathy; BSE; scrapie;
 XX KW feline spongiform encephalopathy; chronic wasting disease;
 XX KW transmissible mink encephalopathy; sterilisation; prion.
 XX XX
 XX OS Unidentified.
 XX XX
 XX PN US2004091474-A1.
 XX XX
 XX PD 13-MAY-2004.
 XX XX
 XX PF 08-JUL-2003; 2003US-00614370.
 XX XX
 XX PR 08-JAN-2001; 2001GB-00000420.

PR 26-FEB-2001; 2001GB-00004696.
 PR 08-JAN-2002; 2002WO-GB000052.
 PR 11-JUL-2002; 2002GB-00016146.
 XX (HEAL-) HEALTH PROTECTION AGENCY.
 XX PA Raven NDH, Sutton JM;
 XX PI WPI; 2004-374912/35.
 XX DR
 XX XX
 PT Inactivating transmissible spongiform encephalopathy (TSE) agent,
 PT involves exposing TSE agent to thermostable proteolytic enzyme such as
 PT subtilisin.
 XX
 XX Example 1; SEQ ID NO 4; 49pp; English.
 XX
 CC The invention relates to a method of inactivating a transmissible
 CC spongiform encephalopathy (TSE) agent. The method involves exposing the
 CC TSE agent to a thermostable proteolytic enzyme such as subtilisin. The
 CC invention is useful for inactivating a transmissible spongiform
 CC encephalopathy (TSE) agent selected from Creutzfeldt-Jacob disease,
 CC variant Creutzfeldt-Jacob disease, Kuru, fatal familial insomnia,
 CC Gerstmann-Strausler-Scheinker syndrome, bovine spongiform encephalopathy
 CC (BSE), scrapie, feline spongiform encephalopathy, chronic wasting disease
 CC and transmissible mink encephalopathy. The invention is useful for
 CC sterilising medical apparatus and for inactivation of TSE agents in
 CC potentially contaminated clinical waste and culled animal material. The
 CC present sequence is a prion mimetic peptide. This sequence is used to
 CC illustrate the method of the invention.
 XX
 SQ Sequence 19 AA;
 Query Match 100.0%; Score 72; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5.4e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CITQYQRESQAYY 13
 Db |||||:|||||
 1 CITQYQRESQAYY 13
 RESULT 9
 AB08378
 ID ABB08378 standard; peptide; 13 AA.
 XX AC ABB08378;
 XX DT 22-APR-2002 (first entry)
 XX DE Mutant immunogenic peptide derived from bovine prion protein.
 XX DE Prion; BSE; bovine spongiform encephalopathy; vCJD;
 KW new variant creutzfeldt jacob disease; scrapie; TSE;
 KW transmissible spongiform encephalopathy; antibody; PrPsc; PrPc; vaccine;
 KW CJD; creutzfeldt jacob disease; cow.
 XX OS Bos taurus.
 XX XX
 FH Key Location/Qualifiers
 FT Misc-difference 6 /note= "wild-type Gln is replaced by Glu."
 FT
 XX EP1158003-A1.
 XX PD 28-NOV-2001.
 XX XX
 XX 23-MAY-2000; 2000EP-00111108.
 XX 23-MAY-2000; 2000EP-00111108.
 XX (BLOO-) BLOOD TRANSFUSION CENT SLOVENIA.
 XX Curin-Serbec;
 PI

XX WPI; 2002-107827/15.
 XX
 PT New antibody, useful in diagnosis and treatment of BSE, CJD, new variant
 PT CJD and other transmissible Spongiform Encephalopathy related diseases,
 PT selectively binds to the infectious form of the prion protein.
 XX
 PS Claim 3; Page 10; 21pp; English.
 XX
 CC The invention relates to an antibody selectively binding to the three
 CC dimensional conformation of the C-terminal of the infectious 'scrapie'
 CC (PrPsc) isoform of the prion protein (or a part), but not binding to the
 CC structure of the C-terminal of the normal cellular (PrPc) isoform of the
 CC prion protein. The antibodies (or functional parts) are useful in the
 CC diagnosis of Bovine Spongiform Encephalopathy (BSE), Creutzfeldt Jacobs
 CC Disease (CJD), new variant form CJD (vCJD) and other Transmissible
 CC Spongiform Encephalopathy (TSE) related diseases e.g. in humans, cows,
 CC sheep etc., since they can differentiate between the infectious (PrPsc)
 CC isoform and the normal cellular (PrPc) isoform of the prion protein. They
 CC are also useful in the treatment of such diseases. They may be included in
 CC pharmaceutical compositions or used to produce drugs or active and/or
 CC passive vaccines against diseases as above. The anti-idiotypic antibodies
 CC of the polypeptides of the invention may also be used to produce drugs or
 CC vaccines against such diseases. The current sequence represents a mutant
 CC immunogenic peptide derived from bovine prion protein C-terminal region
 CC (see AB08377). This sequence is created from the wild-type sequence by
 CC replacement of the Gln residue at position 6 of the peptide with Glu.
 CC This sequence has proven to elicit an immune response sufficiently strong
 CC enough to be capable of easily raising antibodies specifically against
 CC PrPsc
 XX
 SQ Sequence 13 AA;
 Query Match 95.8%; Score 69; DB 5; Length 13;
 Best Local Similarity 92.3%; Pred. No. 1.3e-05;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CITQYQRESQAYY 13
 Db |||||:|||||
 1 CITQYQRESQAYY 13
 RESULT 10
 ADD24246
 ID ADD24246 standard; peptide; 13 AA.
 XX AC ADD24246;
 XX DT 15-JAN-2004 (first entry)
 XX DE Human prion protein PrP peptide 214-226.
 XX KW vaccine composition; virus-like particle; core particle;
 KW first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; anti-inflammatory;
 KW Prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jacob Disease; prion.
 XX OS prion.
 XX PN WO2003059386-A2.
 XX PD 24-JUL-2003.
 XX PF 17-JAN-2003; 2003WO-EP000460.
 XX 18-JAN-2002; 2002US-00050902.
 PR 21-JAN-2002; 2002WO-IB000166.
 PR 08-JUL-2002; 2002US-0393725P.
 PR 18-JUL-2002; 2002US-0396590P.
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 XX PA
 XX XX

PI Bachmann M, Maurer P, Pelliccioli E, Renner WA;
 XX WPI; 2003-598483/56.
 XX
 PT A vaccine composition for preventing or treating prion diseases (e.g.
 PT Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-
 PT phage) and at least one prion protein or peptide bound to the virus-like
 PT particle.
 XX
 PS Disclosure; Page 86; 246pp; English.
 XX
 CC This invention relates to a novel vaccine composition comprising a virus-
 CC like or a core particle with at least one first attachment site and at
 CC least one antigen or antigenic determinant that is a prion protein (Prp)
 CC or its dimer, or a Prp peptide, the antigen or antigenic determinant
 CC being bound to the virus-like or core particle. The vaccine of the
 CC invention may have neuroprotective or antiinflammatory activity. The
 CC composition is useful as a medicament or in manufacturing a medicament
 CC for the treatment or prevention of prion diseases. The prion diseases may
 CC include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
 CC Disease. The present sequence is that of a peptide fragment of a prion
 CC protein which may be used for the production of the vaccine of the
 CC invention.
 XX
 SQ Sequence 13 AA;
 Query Match 95.8%; Score 69; DB 7; Length 13;
 Best Local Similarity 92.3%; Pred. No. 1.3e-05;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CITQYQRESQAYY 13
 Db 1 CITQYQRESQAYY 13
 |||||:|||||
 RESULT 11
 ADC53154
 ID ADC53154 standard; peptide; 15 AA.
 AC ADC53154;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Immunological assay related IgG peptide 2.
 XX
 KW analogue; immunoassay; coupled; antigenic; toxic; infectious;
 KW immunological; IgG.
 XX
 OS Unidentified.
 XX
 XX JP2003111592-A.
 XX
 PD 15-APR-2003.
 XX
 PF 04-OCT-2001; 2001JP-00308464.
 XX
 PR 04-OCT-2001; 2001JP-00308464.
 XX
 XX (MENE-) MENEKI SEIBUTSU KENKYUSHO KK.
 PA
 XX WPI; 2003-601766/57.
 DR
 XX
 PT Novel analog of a test substance to be measured by immunoassay, has
 PT peptide with two antigenic determinants similar to the antigenic
 PT determinants of test substance, coupled to both ends of basic peptide
 PT sequence.
 XX
 XX Example 3; SEQ ID NO 8; 10pp; Japanese.
 PS
 XX The invention relates to a novel immunological analogue of a test
 CC substance to be measured by an immunoassay, which contains a peptide
 CC sequence coupled to both ends of a basic peptide sequence. The peptide
 CC sequence comprises two different antigenic determinants which are similar

CC to the antigenic determinants present in the test substance. The
 CC immunoassay has the advantage of toxic and infectious proteins being
 CC determined safely and simply. This sequence represents an IgG peptide
 CC used in the method of the invention.
 XX
 SQ Sequence 15 AA;
 Query Match 95.8%; Score 69; DB 7; Length 15;
 Best Local Similarity 92.3%; Pred. No. 1.5e-05;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CITQYQRESQAYY 13
 Db 1 CITQYQRESQAYY 13
 |||||:|||||
 RESULT 12
 ABB80955
 ID ABB80955 standard; peptide; 18 AA.
 XX
 AC ABB80955;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Prion E3 region peptide fragment.
 XX
 KW Prion; monoclonal antibody; Mab; antigen; Creutzfeldt-Jakob disease;
 KW scrapie; encephalopathy; immunogen; epitope.
 XX
 OS Homo sapiens.
 XX
 PN EP1213301-A2.
 XX
 PD 12-JUN-2002.
 XX
 PF 10-DEC-2001; 2001EP-00310310.
 XX
 PR 08-DEC-2000; 2000JP-00374145.
 XX
 PA (FJRE) FUJIREBIO INC.
 XX
 PI Kurano Y, Umetani A, Miyakoshi H, Yanagiya T;
 XX
 DR WPI; 2002-550348/59.
 XX
 PT An anti-abnormal type prion monoclonal antibody/ or antigen binding
 PT fragment, which reacts with abnormal type prion but does not react with
 PT normal type.
 XX
 PS Disclosure; Page 4; 12pp; English.
 XX
 CC The invention relates to an anti-abnormal type prion monoclonal antibody
 CC (Mab)/ or antigen binding fragment, which reacts with abnormal type prion
 CC but does not substantially react with normal type prion by antigen-
 CC antibody reaction. The Mab is produced by hybridoma EBBB4S3EBB (FERM BP-
 CC 7808). The invention provides a means of producing antibody to detect
 CC abnormal prion with the possibility of identifying the presence of the
 CC same in disease states such as Creutzfeldt-Jakob disease, scrapie disease
 CC of sheep and transmissible encephalopathy. The present sequence
 CC represents a prion peptide fragment used for constructing an immunogen
 CC for raising anti-abnormal prion Mab
 XX
 SQ Sequence 18 AA;
 Query Match 95.8%; Score 69; DB 5; Length 18;
 Best Local Similarity 92.3%; Pred. No. 1.8e-05;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CITQYQRESQAYY 13
 Db 1 CITQYQRESQAYY 13
 |||||:|||||

RESULT 13
 ADD24243
 ID ADD24243 standard; peptide; 20 AA.
 AC
 AC ADD24243;
 XX
 XX 15-JAN-2004 (first entry)
 DT
 XX Mouse prion protein PrP peptide #2.
 DE
 XX vaccine composition; virus-like particle; core particle;
 KW first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jakob Disease; prion.
 XX
 OS prion.
 OS
 XX WO2003059386-A2.
 PN
 XX 24-JUL-2003.
 PD
 XX 17-JAN-2003; 2003WO-EP000460.
 PF
 XX 18-JAN-2002; 2002US-00050902.
 XX 21-JAN-2002; 2002WO-1B000166.
 PR 08-JUL-2002; 2002US-0393725P.
 PR 18-JUL-2002; 2002US-0396590P.
 XX
 XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
 PA
 XX Bachmann M, Maurer P, Pelliccioli E, Renner WA;
 PI WPI; 2003-598483/56.
 XX
 DR A vaccine composition for preventing or treating prion diseases (e.g.
 XX Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-
 PT phage) and at least one prion protein or peptide bound to the virus-like
 PT particle.
 PT
 XX Disclosure; Page 83; 246pp; English.
 PS
 XX This invention relates to a novel vaccine composition comprising a virus-
 CC like or a core particle with at least one first attachment site and at
 CC least one antigen or antigenic determinant that is a prion protein (PrP)
 CC or its dimer, or a PrP peptide, the antigen or antigenic determinant
 CC being bound to the virus-like or core particle. The vaccine of the
 CC invention may have neuroprotective or antiinflammatory activity. The
 CC composition is useful as a medicament or in manufacturing a medicament
 CC for the treatment or prevention of prion diseases. The prion diseases may
 CC include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
 CC Disease. The present sequence is that of a peptide fragment of a prion
 CC protein which may be used for the production of the vaccine of the
 CC invention.
 XX
 SQ Sequence 20 AA;
 Query Match 94.4%; Score 68; DB 7; Length 20;
 Best Local Similarity 84.6%; Pred. No. 3.1e-05;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTVQYQESQAYY 13
 DB 3 CTVQYQESQAYY 15
 RESULT 14
 ADL15228
 ID ADL15228 standard; peptide; 12 AA.
 XX
 AC ADL15228;
 XX
 XX 20-MAY-2004 (first entry)
 DT

XX Bovine prion protein PrP peptide - SEQ ID 23.
 DE prion; PrPSc; vaccine; Creutzfeldt-Jakob disease; kuru;
 XX Gerstmann-Straussler-Sheinker syndrome; fatal familial insomnia;
 KW transmissible spongiform encephalopathy;
 KW bovine spongiform encephalopathy; BSE; cattle; scrapie; sheep;
 KW chronic wasting; deer; elk; mink; cat; bovine; cow; PrP.
 XX
 OS Bos sp.
 XX
 XX WO2004018511-A2.
 PN
 XX 04-MAR-2004.
 PD
 XX 25-AUG-2003; 2003WO-DK000555.
 PF
 XX 23-AUG-2002; 2002DK-00001245.
 PR
 XX (COPE-) COPENHAGEN BIOTECH ASSETS APS.
 PA
 XX Heegaard P, Jakobsen PH;
 PI WPI; 2004-226799/21.
 DR
 XX Conjugate useful for treating transmissible prion disease, e.g., kuru,
 PT comprising two or more peptides or its fragments optionally linked to
 PT backbone form to non-linear sequences which mimics tertiary structure of
 PT stable prion protein.
 XX
 PS Claim 13; SEQ ID NO 23; 70pp; English.
 XX
 CC The invention relates to a novel conjugate comprising two or more peptide
 CC fragments optionally linked to a backbone where the peptides are
 CC spatially positioned relative to each other to form non-linear sequences
 CC which mimic the tertiary structure of pathogenic prion protein PrPSc-
 CC specific epitopes and have the same or higher degree of conformational
 CC sensitivity to PrPSc. The conjugate of the invention demonstrates
 CC neuroprotective activity and may be useful for producing antibodies
 CC specific for PrPSc for use in medicine, vaccines, high-throughput
 CC screening and as direct probes or reporter substances in assays for
 CC detection of PrPSc. Furthermore, the conjugate and peptides may be useful
 CC for treating and/or preventing Creutzfeldt-Jakob disease, kuru, Gerstmann
 CC -Straussler-Sheinker syndrome, fatal familial insomnia and transmissible
 CC spongiform encephalopathies, such as bovine spongiform encephalopathy
 CC (BSE) in cattle, scrapie in sheep, chronic wasting disease in deer and
 CC elk and transmissible encephalopathies in mink, cat and other animals.
 CC The current sequence is that of a bovine prion protein PrP peptide of the
 CC invention.
 XX
 SQ Sequence 12 AA;
 Query Match 87.5%; Score 63; DB 8; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ITOYQRESQAYY 13
 DB 1 ITOYQRESQAYY 12
 RESULT 15
 ADL15244
 ID ADL15244 standard; peptide; 12 AA.
 XX
 AC ADL15244;
 XX
 XX 20-MAY-2004 (first entry)
 DT
 XX Bovine prion protein PrP peptide - SEQ ID 39.
 DE prion; PrPSc; vaccine; Creutzfeldt-Jakob disease; kuru;
 KW Gerstmann-Straussler-Sheinker syndrome; fatal familial insomnia;
 KW

KW transmissible spongiform encephalopathy;
KW bovine spongiform encephalopathy; BSE; cattle; scrapie; sheep;
KW chronic wasting; deer; elk; mink; cat; bovine; cow; PrP.
XX
OS Bos sp.
XX
PN WO2004018511-A2.
XX
PD 04-MAR-2004.
XX
PF 25-AUG-2003; 2003WO-DK000555.
XX
PR 23-AUG-2002; 2002DK-00001245.
XX
PA (COPE-) COPENHAGEN BIOTECH ASSETS APS.
XX
PI Heegaard P, Jakobsen PH;
XX
DR WPI; 2004-226799/21.
XX
XX Conjugate useful for treating transmissible prion disease, e.g., kuru,
PT comprising two or more peptides or its fragments optionally linked to
PT backbone form to non-linear sequences which mimics tertiary structure of
PT stable prion protein.
XX
PS Claim 15; SEQ ID NO 39; 70pp; English.
XX
XX The invention relates to a novel conjugate comprising two or more peptide
CC fragments optionally linked to a backbone where the peptides are
CC spatially positioned relative to each other to form non-linear sequences
CC which mimic the tertiary structure of pathogenic prion protein PrPSc-
CC specific epitopes and have the same or higher degree of conformational
CC sensitivity to PrPSc. The conjugate of the invention demonstrates
CC neuroprotective activity and may be useful for producing antibodies
CC specific for PrPSc for use in medicine, vaccines, high-throughput
CC screening and as direct probes or reporter substances in assays for
CC detection of PrPSc. Furthermore, the conjugate and peptides may be useful
CC for treating and/or preventing Creutzfeldt-Jakob disease, kuru, Gerstmann
CC -Strausler-Sheinker syndrome, fatal familial insomnia and transmissible
CC spongiform encephalopathies, such as bovine spongiform encephalopathy
CC (BSE) in cattle, scrapie in sheep, chronic wasting disease in deer and
CC elk and transmissible encephalopathies in mink, cat and other animals.
CC The current sequence is that of a bovine prion protein PrP peptide of the
XX invention.
XX
SQ Sequence 12 AA;

Query Match 87.5%; Score 63; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ITOYQRESQAYY 13
Db 1 ITOYQRESQAYY 12
|||||

Search completed: September 15, 2005, 16:38:54
Job time : 122 secs

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OM protein - protein search, using sw model

Run on: September 15, 2005, 16:05:21 ; Search time 24.5 Seconds
(without alignments)
51.054 Million cell updates/sec

Title: US-09-576-724-2

Perfect score: 72
Sequence: 1 CITQYQRESQAYY 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: piri:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	24	33.3	12	2 PH1605	Ig H chain V-D-J r
2	24	33.3	14	2 C40944	hypothetical prote
3	24	33.3	14	2 PT0252	Ig heavy chain CRD
4	23	31.9	13	2 S47358	T-cell antigen rec
5	22	30.6	13	2 S12388	argA protein - Sal
6	22	30.6	15	2 A17340	ribonucleoside-dip
7	22	30.6	18	2 B40741	T-cell receptor be
8	21	29.2	14	2 B83836	hypothetical prote
9	21	29.2	19	2 C32735	thyroglobulin - pl
10	21	29.2	19	2 B32735	thyroglobulin - sh
11	21	29.2	19	2 PH1609	Ig H chain V-D-J r
12	21	29.2	20	2 PX0059	trypsin inhibitor
13	21	29.2	20	2 A47105	dystroglycan - chi
14	21	29.2	20	2 S28405	lamin B receptor -
15	20	27.8	12	2 PH0771	T-cell receptor be
16	20	27.8	13	2 S47381	T-cell antigen rec
17	20	27.8	13	2 S14316	photosystem I 9K c
18	20	27.8	14	2 E49039	T-cell receptor be
19	20	27.8	15	2 PH1613	Ig H chain V-D-J r
20	20	27.8	15	2 PA0062	fumarate hydratase
21	19.5	27.1	19	2 A49254	Tcr delta chain V-
22	19	26.4	10	2 C54226	light-harvesting p
23	19	26.4	14	2 PT0232	Ig heavy chain CRD
24	19	26.4	14	2 PT0254	Ig heavy chain CRD
25	19	26.4	14	2 PH1597	Ig H chain V-D-J r
26	19	26.4	15	2 PA0057	adenylate isopente
27	19	26.4	17	2 I67526	CD33 antigen homol
28	19	26.4	18	2 PQ0022	fixA protein - Rhi
29	19	26.4	18	2 A43334	orf1 5' of aadr -

30	19	26.4	18	2 S54270	GATA-2 protein - A
31	19	26.4	20	2 S06150	photosystem I chai
32	19	26.4	20	2 S27351	lysophospholipase
33	18.5	25.7	12	2 PH0802	T-cell receptor al
34	18	25.0	10	2 A37268	Ig heavy chain C r
35	18	25.0	11	2 S07203	uperolein - frog (
36	18	25.0	12	2 PH1454	T-cell receptor al
37	18	25.0	13	2 A53608	neurotensin - guin
38	18	25.0	13	2 S47373	T-cell antigen rec
39	18	25.0	14	2 PH1608	Ig H chain V-D-J r
40	18	25.0	14	2 PH0762	T-cell receptor be
41	18	25.0	15	2 PH1318	Ig heavy chain DJ
42	18	25.0	15	2 E49037	Tcr delta chain V-
43	18	25.0	16	2 PH1781	T cell receptor al
44	18	25.0	16	2 B44036	collagen alpha 1(X
45	18	25.0	16	2 D89854	conserved hypothet

ALIGNMENTS

RESULT 1

PH1605
Ig H chain V-D-J region (wild-type clone 328) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1605

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
A:Reference number: PH1580; MUID:93301609; PMID:8315387
A:Accession: PH1605

A:Molecule type: DNA

A:Residues: 1-12 <LEV>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 33.3%; Score 24; DB 2; Length 12;
Best Local Similarity 25.0%; Pred. No. 3.5e+02;
Matches 3; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 CITQYQRESQAY 12

DB 1 CARRYREDAMDY 12

RESULT 2

C40944

hypothetical protein (1-phosphofructokinase 5' region) - Xanthomonas campestris pv. cam
C:Species: Xanthomonas campestris pv. campestris
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C:Accession: C40944

R:de Crecy-Lagard, V.; Bouvet, O.M.M.; Lejeune, P.; Danchin, A.

J. Biol. Chem. 266, 18154-18161, 1991

A:Title: Fructose catabolism in Xanthomonas campestris pv. campestris

A:Reference number: A40944; MUID:92011547; PMID:1655739

A:Accession: C40944

A:Molecule type: DNA

A:Residues: 1-14 <DE3>

A:Cross-references: UNIPROT:P45597; GB:M69242; NID:G155366; PIDN:AAA27600.1; PID:G15536
C:Superfamily: fructose phosphotransferase multiphosphoryltransfer protein; phosphotran
sphotransferase system phosphohistidine-containing protein homology

Query Match 33.3%; Score 24; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 QRESQA 11

DB 9 QREGQA 14

RESULT 3

PT0252

IG heavy chain CRD3 region (clone 2-109D) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0252
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PT0222; MUID:91108337; PMID:1899102
 A:Accession: PT0252
 A:Molecule type: DNA
 A:Residues: 1-14 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 24; DB 2; Length 14;
 Best Local Similarity 44.4%; Pred. No. 4.1e+02;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 YQRESQAYY 13
 | | | | |
 DB 4 YYDSGGY 12

RESULT 4

S47358
 T-cell antigen receptor VJ junction beta chain - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S47358
 R:Lehner, P.J.
 submitted to the EMBL Data Library, August 1994
 A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
 A:Reference number: S47355
 A:Accession: S47358
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-13 <LEH>
 A:Cross-references: EMBL:235682; NID:g527453; PIDN:CAA84751.1; PID:g527454
 C:Keywords: T-cell receptor

Query Match 31.9%; Score 23; DB 2; Length 13;
 Best Local Similarity 23.1%; Pred. No. 5.8e+02;
 Matches 3; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CITQYQESQAYY 13
 | | | | |
 DB 1 CASSYYRNQPHF 13

RESULT 5

S12388
 argA protein - Salmonella typhimurium (fragment)
 C:Species: Salmonella typhimurium
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
 C:Accession: S12388
 R:Shyamala, V.; Schneider, E.; Ames, G.P.L.
 EMBO J. 9, 939-946, 1990
 A:Title: Tandem chromosomal duplications: role of REP sequences in the recombination eve
 A:Reference number: S12388; MUID:90183995; PMID:2178927
 A:Accession: S12388
 A:Molecule type: DNA
 A:Residues: 1-13 <SHY>
 C:Genetics:
 A:Gene: argA

Query Match 30.6%; Score 22; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 9e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 YQRESQ 10
 | | | | |
 DB 1 YQRRSK 6

RESULT 6

Al7340
 ribonucleoside-diphosphate reductase (BC 1.17.4.1), adenosylcobalamin-dependent - coryn-
 C:Species: coryneform bacterium ATCC11425
 C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
 C:Accession: Al7340
 R:Tsai, P.K.; Hogenkamp, H.P.C.
 J. Biol. Chem. 255, 1273-1278, 1980
 A:Title: The purification and characterization of an adenosylcobalamin-dependent ribonu
 A:Reference number: Al7340; MUID:80115631; PMID:6986368
 A:Note: Corynebacterium nephridii
 A:Accession: Al7340
 A:Molecule type: protein
 A:Residues: 1-15 <TSA>
 A:Cross-references: UNIPROT:Q7MOK8
 C:Keywords: oxidoreductase

Query Match 30.6%; Score 22; DB 2; Length 15;
 Best Local Similarity 30.0%; Pred. No. 1e+03;
 Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 4 QYQRESQAYY 13
 | | | | |
 DB 6 RFTKENQSAV 15

RESULT 7

B40741
 T-cell receptor beta chain - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
 C:Accession: B40741
 R:Mallick, C.A.; Dudley, E.C.; Viney, J.L.; Owen, M.J.; Hayday, A.C.
 Cell 73, 513-519, 1993
 A:Title: Rearrangement and diversity of T cell receptor beta chain genes in thymocytes:
 A:Reference number: A40741; MUID:93258815; PMID:8387894
 A:Accession: B40741
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-18 <MAL>
 A:Cross-references: GB:S60903; NID:g300356; PIDN:AA826614.1; PID:g300357
 A:Experimental source: thymocytes, clone 1.V5
 A:Note: sequence extracted from NCBI backbone (NCBIN:131689, NCBI:131693)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: T-cell receptor

Query Match 30.6%; Score 22; DB 2; Length 18;
 Best Local Similarity 23.1%; Pred. No. 1.3e+03;
 Matches 3; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CITQYQESQAYY 13
 | | | | |
 DB 3 CASSRDRQDTQYF 15

RESULT 8

B83836
 hypothetical protein BH1490 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C:Accession: B83836
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir-
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: B83836
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-14 <STO>
 A:Cross-references: UNIPROT:Q9KCS9; GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BA0052
 A:Experimental source: strain C-125

C;Genetics:
A;Gene: BHL490

Query Match 29.2%; Score 21; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 YQRESQ 10
| : | : | :
Db 4 YQKEEE 9

RESULT 9

C32735
thyroglobulin - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 09-Jul-2004
C;Accession: C32735
R;Rawitch, A.B.; Litwer, M.R.; Gregg, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.
Biochem. Biophys. Res. Commun. 118, 423-429, 1984
A;Title: The isolation of identical thyroxine containing amino acid sequences from bovin
A;Reference number: A32735; MUID:84153804; PMID:6704086
A;Accession: C32735
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <RAW>
A;Cross-references: UNIPROT:Q7M222
C;Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homol
C;Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis
F;5/Modified site: thyroxine (Tyr) #status predicted

Query Match 29.2%; Score 21; DB 2; Length 19;
Best Local Similarity 44.4%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 ITQYQRESQ 10
| : | : | :
Db 2 IFEYQVDAQ 10

RESULT 10

B32735
thyroglobulin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 09-Jul-2004
C;Accession: B32735
R;Rawitch, A.B.; Litwer, M.R.; Gregg, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.
Biochem. Biophys. Res. Commun. 118, 423-429, 1984
A;Title: The isolation of identical thyroxine containing amino acid sequences from bovin
A;Reference number: A32735; MUID:84153804; PMID:6704086
A;Accession: B32735
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <RAW>
A;Cross-references: UNIPROT:Q7M221
C;Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homol
C;Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis
F;5/Modified site: thyroxine (Tyr) #status predicted

Query Match 29.2%; Score 21; DB 2; Length 19;
Best Local Similarity 44.4%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 ITQYQRESQ 10
| : | : | :
Db 2 IFEYQVDAQ 10

RESULT 11

PH1609
Ig H chain V-D-J region (wild-type clone 336) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1609

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1609

A;Molecule type: DNA

A;Residues: 1-19 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 29.2%; Score 21; DB 2; Length 19;
Best Local Similarity 41.7%; Pred. No. 2e+03;
Matches 5; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 ITQYQRESQAYY 13
| : | : | :
Db 4 IVYYDGSRYYY 15

RESULT 12

PX0059
trypsin inhibitor chain A - Acacia confusa (fragment)
C;Species: Acacia confusa
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 17-Mar-2000
C;Accession: PX0059
R;Lin, J.; Chu, S.; Wu, H.; Heieh, Y.

J. Biochem. 110, 879-883, 1991

A;Title: Trypsin inhibitor from the seeds of Acacia confusa.

A;Reference number: PX0059; MUID:92176160; PMID:1794977

A;Accession: PX0059

A;Molecule type: protein

A;Residues: 1-20 <LIN>

C;Superfamily: plant Kunitz-type proteinase inhibitor

C;Keywords: serine proteinase inhibitor

Query Match 29.2%; Score 21; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 2.2e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 RESQAYY 13
| : | : | :
Db 12 RRGQAYY 18

RESULT 13

A47105
dystroglycan - chicken (fragment)
N;Alternate names: laminin-binding protein 120
C;Species: Gallus gallus (chicken)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47105
R;Gee, S.H.; Blacher, R.W.; Douville, P.J.; Provost, P.R.; Yurchenco, P.D.; Carbonetto, J. Biol. Chem. 268, 14972-14980, 1993
A;Title: Laminin-binding protein 120 from brain is closely related to the dystrophin-as
A;Reference number: A47105; MUID:93315474; PMID:8325873
A;Accession: A47105
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <GEE>
A;Cross-references: UNIPROT:Q9PRM4
A;Experimental source: embryonic brain
A;Note: sequence extracted from NCBI backbone (NCBIP:134982)
C;Keywords: heparin binding

Query Match 29.2%; Score 21; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 QYQRESQAYY 13
| : | : | :
Db 3 QFNNSQLMY 12

RESULT 14

S28405
lamin B receptor - turkey (fragment)
N:Alternate names: inner nuclear membrane protein p58
C:Species: Meleagris gallopavo (common turkey)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S28405
R:Simos, G.; Georgatos, S.D.
EMBO J. 11, 4027-4036, 1992
A:Title: The inner nuclear membrane protein p58 associates in vivo with a p58 kinase and
A:Reference number: S28405; MUID:93010998; PMID:1327755
A:Accession: S28405
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <SIM>
A:Cross-references: UNIPROT:Q7LZ11
C:Keywords: DNA binding; nucleus; receptor; transmembrane protein

Query Match 29.2%; Score 21; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. NO. 2.2e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRESQA 11
|||:
Db 2 QKKSQS 7

RESULT 15

PH0771
T-cell receptor beta chain (PE5.1.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0771
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0771
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: EMBL:X60865; NID:g53624; PIDN:CAA43255.1; PID:g53625
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 27.8%; Score 20; DB 2; Length 12;
Best Local Similarity 37.5%; Pred. NO. 2e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CITQVQRE 8
|:|:
Db 1 CASSPQYE 8

Search completed: September 15, 2005, 16:39:56
Job time : 24.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2005, 15:50:48 ; Search time 621 Seconds
(without alignments)
10.720 Million cell updates/sec

Title: US-09-576-724-2
Perfect score: 72
Sequence: 1 CITQYQRESQAY 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 12050

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 03.4
1: uniprot_sprot.4
2: uniprot_trembl.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	37.5	8	Q8WFR5	Q8wfr5 diadema pau
2	26	36.1	13	Q718T2	Q718t2 newcastle d
3	26	36.1	15	Q7KQF8	Q7kqf8 drosophila
4	24	33.3	9	Q7RSP2	Q7rsp2 plasmodium
5	24	33.3	18	Q7RNN4	Q7rnn4 plasmodium
6	23	31.9	14	Q85CA1	Q85cal strongyloce
7	23	31.9	20	Q9TWV9	Q9twv9 trypanosoma
8	22	30.6	11	P97755	P97755 rattus norv
9	22	30.6	15	Q7MOK8	Q7mok8 corynebacte
10	22	30.6	17	Q9V2X3	Q9v2x3 methanobact
11	22	30.6	20	Q9FUY3	Q9fuy3 zea mays (m
12	21	29.2	8	Q9SM23	Q9sm23 sus scrofa
13	21	29.2	13	Q16141	Q16141 homo sapien
14	21	29.2	13	Q6RSM3	Q6rsm3 coxiella bu
15	21	29.2	14	Q9KCS9	Q9kcs9 bacillus ha
16	21	29.2	15	UC14_MAIZE	P80620 zea mays (m
17	21	29.2	15	UC16_MAIZE	P80622 zea mays (m
18	21	29.2	16	LEC_DELIRE	P83511 delonix reg
19	21	29.2	16	Q6RSJ3	Q6rsj3 coxiella bu
20	21	29.2	17	Q06800	Q06800 saccharomyc
21	21	29.2	17	Q6JW56	Q6jw56 trochodendr
22	21	29.2	19	Q7M2Z1	Q7m2z1 ovis aries
23	21	29.2	19	Q7M2Z2	Q7m2z2 sus scrofa
24	21	29.2	19	Q85AZ5	Q85az5 arapalma gi
25	21	29.2	19	Q85RP4	Q85rp4 arapalma gi
26	21	29.2	20	Q6E807	Q6e807 ovis aries
27	21	29.2	20	Q9S878	Q9s878 petunia hyb
28	21	29.2	20	Q9S7W0	Q9s7w0 neisseria m
29	21	29.2	20	Q7L211	Q7l211 meleagris g
30	21	29.2	20	Q9PRM4	Q9prm4 gallus gall
31	20	27.8	9	Q6VFQ2	Q6vfq2 vibrio fisc

32	20	27.8	11	2	Q800X7	Q800x7 chelydra se
33	20	27.8	12	2	Q9T1J4	Q9t1j4 bacterioph
34	20	27.8	13	2	Q7M1J1	Q7m1j1 spinacia ol
35	20	27.8	13	2	Q936V1	Q936v1 pseudomonas
36	20	27.8	15	2	Q7M4Z3	Q7m4z3 fusarium sp
37	20	27.8	15	2	Q9TRP1	Q9trp1 sus scrofa
38	20	27.8	16	2	Q6USN6	Q6usn6 valeriana c
39	20	27.8	17	2	Q8J167	Q8j167 trichoderma
40	20	27.8	17	2	Q7YRR7	Q7yrr7 sus scrofa
41	20	27.8	19	2	Q8MJY4	Q8mjy4 macaca arct
42	20	27.8	20	2	Q7RHHS	Q7rhh5 plasmodium
43	19	26.4	8	2	Q7RC74	Q7rc74 plasmodium
44	19	26.4	10	2	Q7M0J3	Q7m0j3 marichromat
45	19	26.4	10	2	Q9QVE7	Q9qve7 mus sp. pro

ALIGNMENTS

RESULT 1

Q8WFR5	PRELIMINARY;	PRT;	8 AA.
AC	Q8WFR5;		
DT	01-MAR-2002 (TREMBLrel. 20, Created)		
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
DE	Cytochrome oxidase subunit II (Fragment).		
GN	Name=COII;		
OS	Diadema paucispinum.		
OG	Mitochondrion.		
OC	Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;		
OC	Echinozoa; Euechinozoa; Diadematodea; Diadematodea; Diadematidae;		
OC	Diadema.		
OX	NCBI_TaxID=145530;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21323357; PubMed=11430656;		
RA	Lessios H.A., Kessing B.D., Pearse J.S.;		
RT	"Population structure and speciation in tropical seas: global		
RT	phylogeography of the sea urchin Diadema.";		
RL	Evolution 55:955-975(2001).		
DR	EMBL; AY012959; AAL33852.1; "		
DR	GO; GO:0005739; C:mitochondrion; IEA.		
KW	Mitochondrion.		
FT	NON_TER		
SQ	SEQUENCE 8 AA; 954 MW; C41B173B46DDC2CE CRC64;		

Query Match 37.5%; Score 27; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy	1 CITQYQRE 8
Db	1 CVAQYLEE 8

RESULT 2

Q718T2	PRELIMINARY;	PRT;	13 AA.
ID	Q718T2		
AC	Q718T2;		
DT	05-JUL-2004 (TREMBLrel. 27, Created)		
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)		
DE	Hemagglutinin-neuraminidase (Fragment).		
OS	Newcastle disease virus.		
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;		
OC	Paramyxoviridae; Paramyxovirinae; Avulavirus.		
OX	NCBI_TaxID=11176;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Gould A.R., Hansson E., Selleck K., Kattenbelt J.A., Mackenzie M.,		
RA	Della-Porta A.J.;		
RT	"Newcastle disease virus fusion and hemagglutinin-neuraminidase gene		

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RT motifs as markers for viral lineage.";
RL Avian Pathol. 32:361-373(2003).
DR EMBL; AF542841; AAQ11566.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1628 MW; 685A336009B645BB CRC64;

Query Match 36.1%; Score 26; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 YQRESQAY 12
Db 1 YRRELESY 8

RESULT 3
Q7KQF8 PRELIMINARY; PRT; 15 AA.
ID Q7KQF8
AC Q7KQF8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Homeobox protein (Fragment).
DE Name=NK-4;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=Canton S.;
RA Lee Y., Park T., Schulz R., Kim Y.;
RT "Twist-mediated activation of the NK-4 homeobox gene in the visceral
RT mesoderm of Drosophila requires two distinct clusters of E-box
RT regulatory elements.";
RL J. Biol. Chem. 0:0-0(1997).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=Canton S.;
RA Kim Y., Nirenberg M.;
RT "Drosophila NK-homeobox genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:7716-7720(1989).
DR EMBL; AF004336; AAD09865.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
KW Nuclear protein.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1776 MW; CA5A564B49ADPEFF CRC64;

Query Match 36.1%; Score 26; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 YQRESQAY 13
Db 6 QQQAQSGGY 15

RESULT 4
Q7RSP2 PRELIMINARY; PRT; 9 AA.
ID Q7RSP2;
AC Q7RSP2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Hypothetical protein.
DE Name=PY00313;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1];
RP SEQUENCE FROM N.A.

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RC STRAIN=17XNL;
RX PubMed=12368665; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01000480; EAA22678.1; -.
KW Hypothetical protein.
SQ SEQUENCE 9 AA; 1067 MW; 054CAB46D0505EB0 CRC64;

Query Match 33.3%; Score 24; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CITQY 5
Db 3 CIIQY 7

RESULT 5
Q7RNN4 PRELIMINARY; PRT; 18 AA.
ID Q7RNN4;
AC Q7RNN4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Hypothetical protein (Fragment).
DE Name=PY01782;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368665; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01000480; EAA21149.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2241 MW; 1D1B621B9CB920AE CRC64;

Query Match 33.3%; Score 24; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 RESQAY 12

```

Db 2 RESQFY 7
|||||

RESULT 6

Q85CA1 ID Q85CA1 PRELIMINARY; PRT; 14 AA.
AC Q85CA1; (Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN Name=COII;
OS Strongylocentrotus purpuratus (Purple sea urchin).
OG Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22707965; PubMed=12823452;
RA Biermann C.H., Kessing B.D., Palumbi S.R.;
RT "Phylogeny and development of marine model species: strongylocentrotid
sea urchins."
RL Evol. Dev. 5:360-371(2003).
DR EMBL; AY221017; AAP21733.1;
DR EMBL; AY221018; AAP21736.1;
DR GO; GO:0005739; C.mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1820 MW; 2CB850A51B616CD3 CRC64;

Query Match 31.9%; Score 23; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 2.6e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ITQYQRE 8
:|:|:
Db 8 VTQYLEE 14

RESULT 7

Q9TWV9 ID Q9TWV9 PRELIMINARY; PRT; 20 AA.
AC Q9TWV9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Histone A (Fragment).
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE.
RX MEDLINE=93064852; PubMed=1437281;
RA Bender K., Betschart B., Schaller J., Kamper U., Hecker H.;
RT "Sequence differences between histones of procyclic Trypanosoma brucei
brucei and higher eukaryotes."
RL Parasitology 105:97-104(1992).
SQ SEQUENCE 20 AA; 2498 MW; CE0BC1489FC69BF8 CRC64;

Query Match 31.9%; Score 23; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.8e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ITQYQRES 9
:|:|:
Db 1 IXQFQEST 8

RESULT 8

P97755

ID P97755 PRELIMINARY; PRT; 11 AA.
AC P97755;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Secretogranin II (SGII) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96343805; PubMed=8756552; DOI=10.1210/en.137.9.3815;
RA Jones L.C., Day R.N., Pittler S.J., Valentine D.L., Scammell J.G.;
RT "Cell-specific expression of the rat secretogranin II promoter."
RL Endocrinology 137:3815-3822(1996).
DR EMBL; AF107301; -; NOT_ANNOTATED_CDS.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1298 MW; 3E4E8DA446C1B5A7 CRC64;

Query Match 30.6%; Score 22; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 TOYQRE 8
:|:|:
Db 6 TQYKTE 11

RESULT 9

Q7MOK8 ID Q7MOK8 PRELIMINARY; PRT; 15 AA.
AC Q7MOK8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ribonucleoside-diphosphate reductase (EC 1.17.4.1), adenosylcobalamin-
dependent (Fragment).
OS Corynebacterium nephridii.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1722;
RN [1]
RP SEQUENCE.
RX MEDLINE=80115631; PubMed=6986368;
RA Tsai P.K., Hogenkamp H.P.C.;
RT "The purification and characterization of an adenosylcobalamin-
dependent ribonucleoside diphosphate reductase from Corynebacterium
nephridii."
RL J. Biol. Chem. 255:1273-1278(1980).
DR PIR; A17340; A17340.
DR GO; GO:0004748; F:ribonucleoside-diphosphate reductase activity; IEA.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1901 MW; 99C418699F3EBB18 CRC64;

Query Match 30.6%; Score 22; DB 2; Length 15;
Best Local Similarity 30.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 4 QYQRESQAY 13
:|:|:|:
Db 6 RETKENQSA 15

RESULT 10

Q9V2X3 ID Q9V2X3 PRELIMINARY; PRT; 17 AA.
AC Q9V2X3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RNA polymerase subunit B' (Fragment).
OS Methanobacterium thermoformicum.

OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 RN NCBI_TaxID=145262;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88198019; PubMed=2834336;
 RA Schallenberg J., Moes M., Truss M., Reiser W., Thomm M., Stetter K.O.,
 RA Klein A.;
 RT "Cloning and physical mapping of RNA polymerase genes from
 RT Methanobacterium thermoautotrophicum and comparison of homologues and
 RT gene orders with those of RNA polymerase genes from other methanogenic
 RT archaeobacteria.";
 RL J. Bacteriol. 170:2247-2253(1988).
 DR EMBL; M20391; AAA72654.1; -.
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 2137 MW; 0C03CD9E6D780560 CRC64;

Query Match 30.6%; Score 22; DB 2; Length 17;
 Best Local Similarity 36.4%; Pred. No. 4.9e+03;
 Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 ITOYQRESQAY 12
 ||| :|
 Db 3 ITHYPENHEIY 13

RESULT 11
 Q9FUY3 PRELIMINARY; PRT; 20 AA.
 AC Q9FUY3;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MADS-box protein (Fragment).
 GN Name=tkz-1;
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Young leaf;
 RA Ermishev V.Y., Zbrodina M.V., Karyagina A.S., Naroditsky B.S.,
 RA Khavkin E.E.;
 RT "An unusual K-box sequence of a maize MADS-box gene.";
 RL Russ. J. Plant Physiol. 47:555-557(2000).
 DR EMBL; AF276682; AAG10438.1; -.
 FT NON_TER 1 1
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2477 MW; 0DFD32A46903C4D0 CRC64;

Query Match 30.6%; Score 22; DB 2; Length 20;
 Best Local Similarity 80.0%; Pred. No. 5.8e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 YQRES 9
 ||| :|
 Db 1 YQES 5

RESULT 12
 Q95M23 PRELIMINARY; PRT; 8 AA.
 AC Q95M23;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Na+/K+ ATPase alpha 1 subunit (EC 3.6.1.37) (Fragment).
 GN Name=ATP1A1;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Pietrain;
 RA Blazkova P., Stratil A., Peelman L.J., Van Poucke M., Reiner G.,
 RA Geldermann H., Kopecky M.;
 RT "Linkage assignments of the porcine ATP1A1 and IVL genes, and RH
 RT mapping of ATP1A1, ATP1B1, V-ATPase (CGI-11) and IVL to chromosome
 RT 4.";
 RL Anim. Genet. 33:235-237(2002).
 DR EMBL; AJ344138; CAC51422.1; -.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 KW Hydrolase.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 1117 MW; 604B41AB133B02D3 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 ESQAYY 13
 ||| :|
 Db 3 EKETTY 8

RESULT 13
 Q16141 PRELIMINARY; PRT; 13 AA.
 AC Q16141;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Mutant DNA polymerase beta (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=94220089; PubMed=7545922;
 RA Sadakane Y., Maeda K., Kuroda Y., Hori K.;
 RT "Identification of mutations in DNA polymerase beta mRNAs from
 RT patients with Werner syndrome.";
 RL Biochem. Biophys. Res. Commun. 200:219-225(1994).
 DR EMBL; S69873; AAD14051.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 13 AA; 1568 MW; D88C62798C9542CD CRC64;

Query Match 29.2%; Score 21; DB 2; Length 13;
 Best Local Similarity 37.5%; Pred. No. 5.5e+03;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 YQRESQAY 12
 ||| :|
 Db 1 FRDSAVY 8

RESULT 14
 Q6RSM3 PRELIMINARY; PRT; 13 AA.
 AC Q6RSM3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Coccidia burnetii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
 OC Cocciliaceae; Coccidia.
 OX NCBI_TaxID=777;
 [1]
 RN SEQUENCE FROM N.A.
 RA Glazunova O., Roux V., Raoult D.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY494720; AAR87444.1; -
 DR EMBL; AY494721; AAR87446.1; -
 DR EMBL; AY494722; AAR87448.1; -
 DR EMBL; AY494723; AAR87450.1; -
 DR EMBL; AY494724; AAR87452.1; -
 DR EMBL; AY494725; AAR87454.1; -
 DR EMBL; AY494726; AAR87456.1; -
 DR EMBL; AY494727; AAR87458.1; -
 DR EMBL; AY494728; AAR87460.1; -
 DR EMBL; AY494729; AAR87462.1; -
 DR EMBL; AY494730; AAR87464.1; -
 DR EMBL; AY494731; AAR87466.1; -
 DR EMBL; AY494732; AAR87468.1; -
 DR EMBL; AY494733; AAR87470.1; -
 DR EMBL; AY494719; AAR87442.1; -
 KW Hypothetical protein.
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1519 MW; 877F7F8C02FD321 CRC64;
 Query Match 29.2%; Score 21; DB 2; Length 13;
 Best Local Similarity 80.0%; Pred. No. 5.5e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRESQ 10
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 DB 8 QRETQ 12

RESULT 15
 Q9KCS9 PRELIMINARY; PRT; 14 AA.
 AC Q9KCS9;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE BH150 protein.
 GN OrderedLocusNames=BH1490;
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125;
 RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fuji P., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
 RT halodurans and genomic sequence comparison with Bacillus subtilis.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL; AP001512; BAB05209.1; -
 DR PIR; B83836; B83836.
 KW Complete proteome.
 SQ SEQUENCE 14 AA; 1722 MW; 7036BE9FB869221B CRC64;

Query Match 29.2%; Score 21; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 6e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 YQRESQ 10
 |||:
 DB 4 YQKEE 9

Search completed: September 15, 2005, 16:34:24
 Job time : 622.5 secs

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OM protein - protein search, using sw model

Run on: September 15, 2005, 15:23:47 ; Search time 37 Seconds
(without alignments)
26.228 Million cell updates/sec

Title: US-09-576-724-2

Perfect score: 72
Sequence: 1 CITQYQRESQAYY 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 196327

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	100.0	13	4	US-09-380-015B-9
2	72	100.0	15	1	US-08-244-701B-48
3	72	100.0	15	3	US-09-076-721-48
4	72	100.0	17	3	US-09-353-348-3
5	34	47.2	16	3	US-08-916-246-5
6	34	47.2	16	4	US-09-949-186-5
7	31	43.1	12	6	US-09-353-348-1
8	30	41.7	12	6	US-09-353-348-1
9	30	41.7	12	6	US-09-353-348-1
10	29	40.3	14	2	US-08-750-856A-11
11	29	40.3	14	1	US-08-375-100-10
12	27	37.5	14	1	US-08-465-391A-313
13	27	37.5	14	1	US-08-465-391A-332
14	27	37.5	14	2	US-08-464-538B-311
15	27	37.5	14	2	US-08-464-538B-331
16	27	37.5	14	2	US-08-463-076B-26
17	27	37.5	14	2	US-08-463-076B-335
18	27	37.5	17	4	US-09-459-958-4
19	27	37.5	18	1	US-08-383-474B-312
20	27	37.5	18	1	US-08-465-391A-332
21	27	37.5	18	2	US-08-464-538B-330
22	27	37.5	18	2	US-08-463-076B-333
23	27	37.5	18	4	US-09-428-082B-903
24	27	37.5	20	1	US-08-190-788A-268
25	27	37.5	20	1	US-08-383-474B-271
26	27	37.5	20	1	US-08-465-391A-268
27	27	37.5	20	2	US-08-464-538B-268

28	27	37.5	20	2	US-08-463-076B-322	Sequence 322, App
29	27	37.5	20	4	US-09-428-082B-887	Sequence 887, App
30	27	37.5	20	4	US-09-834-759-535	Sequence 535, App
31	26	36.1	8	3	US-08-335-733D-71	Sequence 71, Appl
32	26	36.1	12	2	US-08-726-306A-140	Sequence 140, App
33	26	36.1	13	2	US-08-572-951-19	Sequence 19, Appl
34	26	36.1	13	2	US-08-572-951-20	Sequence 20, Appl
35	26	36.1	13	2	US-08-572-951-40	Sequence 40, Appl
36	26	36.1	19	3	US-09-307-621-12	Sequence 12, Appl
37	26	36.1	19	3	US-09-307-621-14	Sequence 14, Appl
38	26	36.1	19	3	US-09-307-621-16	Sequence 16, Appl
39	26	36.1	19	4	US-09-205-258-487	Sequence 487, App
40	26	36.1	20	2	US-08-637-759B-459	Sequence 459, App
41	26	36.1	20	3	US-08-871-355A-459	Sequence 459, App
42	26	36.1	20	3	US-08-335-865J-19	Sequence 19, Appl
43	26	36.1	20	3	US-09-201-945-459	Sequence 459, App
44	26	36.1	20	4	US-09-471-276-1471	Sequence 1471, Ap
45	25	34.7	8	3	US-08-335-733D-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1

US-09-380-015B-9
; Sequence 9, Application US/09380015B
; Patent No. 6765088
; GENERAL INFORMATION:
; APPLICANT: Carsten Korth
; TITLE OF INVENTION: Immunological Detection of Prions
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kanton Zuerich vertreten durch die Erziehungsdirektion
; STREET: Walchetur
; CITY: Zuerich
; STATE: Zuerich
; COUNTRY: Switzerland
; ZIP: CH-8090
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/380,015B
; FILING DATE: 23-Aug-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 97102837.8
; FILING DATE: 21-FEB-1997
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-380-015B-9

Query Match 100.0%; Score 72; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.3e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYQRESQAYY 13

Db 1 CITQYQRESQAYY 13

RESULT 2

US-08-244-701B-48
; Sequence 48, Application US/08244701B

```
; Patent No. 5773572
; GENERAL INFORMATION:
; APPLICANT: Fishleigh, Robert V.
; APPLICANT: Robson, Barry
; APPLICANT: Mee, Roger P.
; TITLE OF INVENTION: Fragments of Prion Proteins
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,701B
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Fanucci, Allan A.
; REGISTRATION NUMBER: 30,256
; REFERENCE/DOCKET NUMBER: 8080-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-244-701B-48

Query Match 100.0%; Score 72; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYQRESQAYY 13
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Db 1 CITQYQRESQAYY 13

RESULT 3
US-09-076-721-48
; Sequence 48, Application US/09076721
; Patent No. 6379905
; GENERAL INFORMATION:
; APPLICANT: Fishleigh, Robert V.
; APPLICANT: Robson, Barry
; APPLICANT: Mee, Roger P.
; TITLE OF INVENTION: Fragments of Prion Proteins
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/076,721
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Fanucci, Allan A.
; REGISTRATION NUMBER: 30,256
; REFERENCE/DOCKET NUMBER: 8080-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-244-701B-48

Query Match 100.0%; Score 72; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYQRESQAYY 13
| | | | |
Db 1 CITQYQRESQAYY 13

RESULT 3
US-09-076-721-48
; Sequence 48, Application US/09076721
; Patent No. 6379905
; GENERAL INFORMATION:
; APPLICANT: Fishleigh, Robert V.
; APPLICANT: Robson, Barry
; APPLICANT: Mee, Roger P.
; TITLE OF INVENTION: Fragments of Prion Proteins
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/076,721
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Fanucci, Allan A.
; REGISTRATION NUMBER: 30,256
; REFERENCE/DOCKET NUMBER: 8080-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-244-701B-48

Query Match 100.0%; Score 72; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYQRESQAYY 13
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Db 1 CITQYQRESQAYY 13

RESULT 4
US-09-353-348-3
; Sequence 3, Application US/09353348
; Patent No. 6261790
; GENERAL INFORMATION:
; APPLICANT: O'Rourke, Katherine I.
; TITLE OF INVENTION: Monoclonal Antibodies and Antibody Cocktail for
; TITLE OF INVENTION: Detection of Prion Protein as an Indication of
; TITLE OF INVENTION: Transmissible Spongiform Encephalopathies
; FILE REFERENCE: ORourke
; CURRENT APPLICATION NUMBER: US/09/353,348
; CURRENT FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Ovis aries
US-09-353-348-3

Query Match 100.0%; Score 72; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYQRESQAYY 13
| | | | |
Db 1 CITQYQRESQAYY 13

RESULT 5
US-08-916-246-5
; Sequence 5, Application US/08916246
; Patent No. 6323020
; GENERAL INFORMATION:
; APPLICANT: Perryman, Lance E.
; APPLICANT: Jaemer, Douglas P.
; APPLICANT: Riggs, Michael W.
; APPLICANT: McGuire, Travis C.
; TITLE OF INVENTION: NEUTRALIZATION-SENSITIVE EPITOPES OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Kenneth Sibley, Myers Bigel Sibley & Sajovec
STREET: PO BOX 37428
CITY: Raleigh
STATE: No. 6323020th Carolina
COUNTRY: USA
ZIP: 27627
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,246
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051-405
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1400
TELEFAX: 919-854-1401
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-916-246-5

Query Match 47.2%; Score 34; DB 3; Length 16;
Best Local Similarity 85.7%; Pred. No. 7.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RESQAYY 13
Db 1 KESQAYY 7

RESULT 6
US-09-949-186-5
; Sequence 5, Application US/09949186
; Patent No. 6759048
; GENERAL INFORMATION:
; APPLICANT: Perryman, Lance E
; APPLICANT: Jaemer, Douglas P.
; APPLICANT: Riggs, Michael W.
; APPLICANT: McGuire, Travis C.
; TITLE OF INVENTION: NEUTRALIZATION-SENSITIVE EPITOPES OF CRYPTOSPORIDIUM PARVUM
; FILE REFERENCE: 5051.405DV
; CURRENT APPLICATION NUMBER: US/09/949,186
; CURRENT FILING DATE: 2001-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-949-186-5

Query Match 47.2%; Score 34; DB 4; Length 16;
Best Local Similarity 85.7%; Pred. No. 7.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RESQAYY 13
Db 1 KESQAYY 7

RESULT 7

US-09-353-348-1
; Sequence 1, Application US/09353348
; Patent No. 6261790
; GENERAL INFORMATION:
; APPLICANT: O'Rourke, Katherine I.
; TITLE OF INVENTION: Monoclonal Antibodies and Antibody Cocktail for
; TITLE OF INVENTION: Detection of Prion Protein as an Indication of
; TITLE OF INVENTION: Transmissible Spongiform Encephalopathies
; FILE REFERENCE: O'Rourke
; CURRENT APPLICATION NUMBER: US/09/353,348
; CURRENT FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Ovis aries
US-09-353-348-1

Query Match 43.1%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 QYQRES 9
Db 1 QYQRES 6

RESULT 8
5210075-22
; Patent No. 5210075
; APPLICANT: SCHOLTZ, WOLFGANG; CHIANG, SHIU-LANG; NAGARAJAN,
; GOBI; LOBL, THOMAS J.
; TITLE OF INVENTION: INTERLEUKIN 6 ANTAGONIST PEPTIDES
; NUMBER OF SEQUENCES: 69
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,868
; FILING DATE: 16-FEB-1990
; SEQ ID NO: 22
; LENGTH: 12
5210075-22

Query Match 41.7%; Score 30; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TQYQRESQAY 12
Db 3 SQYQSQSQLF 12

RESULT 9
5210075-22
; Patent No. 5210075
; APPLICANT: SCHOLTZ, WOLFGANG; CHIANG, SHIU-LANG; NAGARAJAN,
; GOBI; LOBL, THOMAS J.
; TITLE OF INVENTION: INTERLEUKIN 6 ANTAGONIST PEPTIDES
; NUMBER OF SEQUENCES: 69
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,868
; FILING DATE: 16-FEB-1990
; SEQ ID NO: 22
; LENGTH: 12
5210075-22

Query Match 41.7%; Score 30; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 TQYQRESQAY 12
Db 3 SQYQSQSQLF 12

RESULT 10
US-08-750-856A-11
; Sequence 11, Application US/08750856A
; Patent No. 5858672
; GENERAL INFORMATION:
; APPLICANT: SONIGO, PIERRE
; APPLICANT: PANCINO, GIANFRANCO
; APPLICANT: PETERHANS, ERNST
; APPLICANT: BERTONI, GUISEPPE
; TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS AND CORRESPONDING
; TITLE OF INVENTION: PEPTIDE FRAGMENTS FROM THE CAPRINE ARTHRITIS-ENCEPHALITIS
; TITLE OF INVENTION: VIRUS (CEAV) GENOME, AND USES THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C. JEFFERSON DAVIS HIGHWAY, SUITE 400
; STREET: 1755 S. ARLINGTON
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,856A
; FILING DATE: 30-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/07933
; FILING DATE: 28-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 917-052-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-750-856A-11

Query Match 40.3%; Score 29; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 56;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 QYQRESQAY 12
Db 5 QWERELQGY 13

RESULT 11
US-08-375-100-10
; Sequence 10, Application US/08375100
; Patent No. 5750332
; GENERAL INFORMATION:
; APPLICANT: Robey, Frank A.
; APPLICANT: Harris-Kelson, Tracy A.
; APPLICANT: Robert-Guroff, Marjorie
; TITLE OF INVENTION: PEPTOMERS WITH ENHANCED IMMUNOGENICITY
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco

STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,100
FILING DATE: 19-JAN-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 15280-190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-375-100-10

Query Match 40.3%; Score 29; DB 1; Length 18;
Best Local Similarity 50.0%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 ITQYQRESQAY 13
Db 6 INMWQVQAMV 17

RESULT 12
US-08-465-391A-313
; Sequence 313, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Phillip R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,391A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5786331viel, Vern
REGISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 313:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 13
OTHER INFORMATION: /note= "Xaa is Azetidine."
NAME/KEY: Region
LOCATION: 14
OTHER INFORMATION: /note= "C-terminal Tyr is amidated."
US-08-465-391A-313
Query Match 37.5%; Score 27; DB 1; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 ESOAYY 13
Db 5 ESNAYY 10
RESULT 13
US-08-465-391A-333
Sequence 333, Application US/08465391A
Patent No. 5786331
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.
APPLICANT: Bovy, Phillip R.
APPLICANT: Leahy, Ellen M.
APPLICANT: Pottorf, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 405
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,391A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223

FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5786331viel, Vern
REGISTRATION NUMBER: 32,483
REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 333:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 14
OTHER INFORMATION: /note= "Xaa is tyrosinamide."
US-08-465-391A-333
Query Match 37.5%; Score 27; DB 1; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 ESOAYY 13
Db 5 ESNAYY 10
RESULT 14
US-08-464-538B-311
Sequence 311, Application US/08464538B
Patent No. 5861476
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Yanofsky, Stephen D.
APPLICANT: Baldwin, David
APPLICANT: Jacobs, Jeff W.
APPLICANT: Bovy, Phillip R.
APPLICANT: Leahy, Ellen M.
APPLICANT: Pottorf, Richard S.
TITLE OF INVENTION: Peptides and Compounds That Bind to the
TITLE OF INVENTION: IL-1 Receptor
NUMBER OF SEQUENCES: 402
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,538B
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,474
FILING DATE: 01-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,788
FILING DATE: 02-FEB-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223

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; REFERENCE/DOCKET NUMBER: 16528A-001810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 311:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 13
; OTHER INFORMATION: /note= "Xaa is Azetidine."
; FEATURE:
; NAME/KEY: Region
; LOCATION: 14
; OTHER INFORMATION: /note= "C-terminal Tyr is amidated."
US-08-464-538B-311

Query Match 37.5%; Score 27; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ESQAYY 13
Db 5 ESNAVY 10

RESULT 15
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; Sequence 311, Application US/08464538B
; Patent No. 5861476
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Phillippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,538B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528A-001810

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 331:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 14
; OTHER INFORMATION: /note= "Xaa is tyrosinamide."
US-08-464-538B-331

Query Match 37.5%; Score 27; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ESQAYY 13
Db 5 ESNAVY 10

Search completed: September 15, 2005, 15:50:32
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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23.982 Million cell updates/sec

Title: US-09-576-724-2

Perfect score: 72

Sequence: 1 CITQYQESQAYY 13

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Searched: 1812044 seqs, 404927589 residues

Total number of hits satisfying chosen parameters: 361688

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	72	100.0	15	US-10-116-061-48
2	72	100.0	19	US-10-614-370-4
3	72	100.0	19	US-10-508-296-8
4	37	51.4	12	US-09-791-378-590
5	37	51.4	12	US-09-791-377-590
6	31	43.1	13	US-09-853-253-26
7	31	43.1	13	US-10-921-371-26
8	31	43.1	15	US-09-853-253-25
9	31	43.1	15	US-10-921-371-25
10	31	43.1	17	US-10-403-938-68
11	30	41.7	18	US-10-022-066-91
				Sequence 48, Appl
				Sequence 4, Appl
				Sequence 8, Appl
				Sequence 590, App
				Sequence 590, App
				Sequence 26, Appl
				Sequence 26, Appl
				Sequence 25, Appl
				Sequence 25, Appl
				Sequence 68, Appl
				Sequence 91, Appl

12	41.7	18	14	US-10-022-066-92	Sequence 92, Appl
13	41.7	20	17	US-10-490-326-45	Sequence 45, Appl
14	28	10	14	US-10-192-869-7	Sequence 7, Appl
15	28	38.9	17	US-10-195-730-375	Sequence 375, App
16	28	38.9	17	US-10-799-747-375	Sequence 375, App
17	28	38.9	17	US-10-979-183-375	Sequence 375, App
18	28	38.9	20	US-10-776-013-255	Sequence 255, App
19	28	38.9	20	US-10-776-013-255	Sequence 616, App
20	27	37.5	14	US-10-807-837-60	Sequence 60, Appl
21	27	37.5	16	US-11-066-697-1241	Sequence 1241, Ap
22	27	37.5	17	US-10-225-322-4	Sequence 4, Appl
23	27	37.5	17	US-10-703-714-38	Sequence 38, Appl
24	27	37.5	17	US-10-703-714-50	Sequence 50, Appl
25	27	37.5	17	US-10-972-135A-80	Sequence 80, Appl
26	27	37.5	18	US-10-142-238A-51	Sequence 51, Appl
27	27	37.5	18	US-10-609-217-903	Sequence 903, App
28	27	37.5	18	US-10-632-388-903	Sequence 903, App
29	27	37.5	18	US-10-651-723-903	Sequence 903, App
30	27	37.5	18	US-10-645-761-903	Sequence 903, App
31	27	37.5	18	US-10-666-696-903	Sequence 903, App
32	27	37.5	18	US-10-653-048-903	Sequence 903, App
33	27	37.5	18	US-10-612-468A-153	Sequence 153, App
34	27	37.5	18	US-10-612-468A-161	Sequence 161, App
35	27	37.5	18	US-10-645-784-903	Sequence 903, App
36	27	37.5	18	US-10-938-992-24	Sequence 24, Appl
37	27	37.5	18	US-10-938-992-50	Sequence 22, Appl
38	27	37.5	18	US-11-093-103-22	Sequence 50, Appl
39	27	37.5	18	US-11-093-103-33	Sequence 33, Appl
40	27	37.5	20	US-09-834-759-535	Sequence 535, App
41	27	37.5	20	US-10-007-805-535	Sequence 535, App
42	27	37.5	20	US-10-076-622-535	Sequence 535, App
43	27	37.5	20	US-10-076-622-598	Sequence 598, App
44	27	37.5	20	US-10-124-805-535	Sequence 535, App
45	27	37.5	20	US-10-124-805-598	Sequence 598, App

ALIGNMENTS

RESULT 1

US-10-116-061-48
; Sequence 48, Application US/10116061
; Publication No. US20030199013A1
; GENERAL INFORMATION:
; APPLICANT: Fishleigh, Robert V.
; Robson, Barry
; Mee, Roger P.
; TITLE OF INVENTION: Fragments of Prion Proteins
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/10/116,061
; FILING DATE: 05-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,701B
; FILING DATE: 02-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fanucci, Allan A.
; REGISTRATION NUMBER: 30,256
; REFERENCE/DOCKET NUMBER: 8080-007
; TELECOMMUNICATION INFORMATION:

```
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-8864/9741
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 48:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-116-061-48

Query Match 100.0%; Score 72; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYQRESQAYY 13
| | | | | | | | | | | | |
Db 1 CITQYQRESQAYY 13

RESULT 2
US-10-614-370-4
/ Sequence 4, Application US/10614370
/ Publication No. US20040091474A1
/ GENERAL INFORMATION:
/ APPLICANT: Raven, Neil David Hammond
/ TITLE OF INVENTION: Degradation and Detection of TSE Infectivity
/ FILE REFERENCE: 1581.0990001
/ CURRENT APPLICATION NUMBER: US/10/614,370
/ CURRENT FILING DATE: 2003-07-08
/ PRIOR APPLICATION NUMBER: GB 0104696.0
/ PRIOR FILING DATE: 2001-02-26
/ PRIOR APPLICATION NUMBER: GB 0100420.9
/ PRIOR FILING DATE: 2001-01-08
/ PRIOR APPLICATION NUMBER: GB 0216146.1
/ PRIOR FILING DATE: 2002-07-11
/ PRIOR APPLICATION NUMBER: PCT/GB02/00052
/ PRIOR FILING DATE: 2002-01-08
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-10-614-370-4

Query Match 100.0%; Score 72; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYQRESQAYY 13
| | | | | | | | | | | | |
Db 1 CITQYQRESQAYY 13

RESULT 3
US-10-508-296-8
/ Sequence 8, Application US/10508296
/ Publication No. US20050163776A1
/ GENERAL INFORMATION:
/ APPLICANT: Microbiological Research Authority
/ APPLICANT: Raven, Neil
/ APPLICANT: Sutton, John
/ APPLICANT: Murdoch, Heather
/ TITLE OF INVENTION: Treatment of TSE Infection
/ FILE REFERENCE: GMS/CMS/24416WO
/ CURRENT APPLICATION NUMBER: US/10/508,296
/ CURRENT FILING DATE: 2004-09-20

/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-8864/9741
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 48:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-116-061-48

Query Match 100.0%; Score 72; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYQRESQAYY 13
| | | | | | | | | | | | |
Db 1 CITQYQRESQAYY 13

RESULT 2
US-10-614-370-4
/ Sequence 4, Application US/10614370
/ Publication No. US20040091474A1
/ GENERAL INFORMATION:
/ APPLICANT: Raven, Neil David Hammond
/ TITLE OF INVENTION: Degradation and Detection of TSE Infectivity
/ FILE REFERENCE: 1581.0990001
/ CURRENT APPLICATION NUMBER: US/10/614,370
/ CURRENT FILING DATE: 2003-07-08
/ PRIOR APPLICATION NUMBER: GB 0104696.0
/ PRIOR FILING DATE: 2001-02-26
/ PRIOR APPLICATION NUMBER: GB 0100420.9
/ PRIOR FILING DATE: 2001-01-08
/ PRIOR APPLICATION NUMBER: GB 0216146.1
/ PRIOR FILING DATE: 2002-07-11
/ PRIOR APPLICATION NUMBER: PCT/GB02/00052
/ PRIOR FILING DATE: 2002-01-08
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-10-614-370-4

Query Match 100.0%; Score 72; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYQRESQAYY 13
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Db 1 CITQYQRESQAYY 13

RESULT 3
US-10-508-296-8
/ Sequence 8, Application US/10508296
/ Publication No. US20050163776A1
/ GENERAL INFORMATION:
/ APPLICANT: Microbiological Research Authority
/ APPLICANT: Raven, Neil
/ APPLICANT: Sutton, John
/ APPLICANT: Murdoch, Heather
/ TITLE OF INVENTION: Treatment of TSE Infection
/ FILE REFERENCE: GMS/CMS/24416WO
/ CURRENT APPLICATION NUMBER: US/10/508,296
/ CURRENT FILING DATE: 2004-09-20

/ PRIOR APPLICATION NUMBER: GB 0206584.5
/ PRIOR FILING DATE: 2002-03-20
/ PRIOR APPLICATION NUMBER: GB 0216098.4
/ PRIOR FILING DATE: 2002-07-11
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 8
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-10-508-296-8

Query Match 100.0%; Score 72; DB 18; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYQRESQAYY 13
| | | | | | | | | | | | |
Db 1 CITQYQRESQAYY 13

RESULT 4
US-09-791-378-590
/ Sequence 590, Application US/09791378
/ Patent No. US20020142303A1
/ GENERAL INFORMATION:
/ APPLICANT: Parekh, Rajesh
/ TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
/ FILE REFERENCE: 9195-061-999
/ CURRENT APPLICATION NUMBER: US/09/791,378
/ CURRENT FILING DATE: 2001-02-23
/ PRIOR APPLICATION NUMBER: 09/750,395
/ PRIOR FILING DATE: 2000-12-28
/ NUMBER OF SEQ ID NOS: 677
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 590
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ OTHER INFORMATION: Synthetic
US-09-791-378-590

Query Match 51.4%; Score 37; DB 9; Length 12;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYQYR 7
| | | | | | |
Db 6 CITQYQYR 12

RESULT 5
US-09-791-377-590
/ Sequence 590, Application US/09791377
/ Publication No. US20040110938A1
/ GENERAL INFORMATION:
/ APPLICANT: Parekh, Rajesh
/ TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
/ FILE REFERENCE: 9195-060-999
/ CURRENT APPLICATION NUMBER: US/09/791,377
/ CURRENT FILING DATE: 2001-02-23
/ PRIOR APPLICATION NUMBER: 09/750,395
/ PRIOR FILING DATE: 2000-12-28
/ NUMBER OF SEQ ID NOS: 677
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 590
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ OTHER INFORMATION: Synthetic
US-09-791-377-590
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Query Match      51.4%; Score 37; DB 11; Length 12;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYQR 7
Db 6 CITQYR 12

RESULT 6
US-09-853-253-26
; Sequence 26, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: (13)...(13)
US-09-853-253-26

Query Match      43.1%; Score 31; DB 9; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QYQRESQA 11
Db 5 QYQHSQA 12

RESULT 7
US-10-921-371-26
; Sequence 26, Application US/10921371
; Publication No. US20050048618A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/10/921,371
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US/09/853,253
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: (13)...(13)
US-10-921-371-26

Query Match      43.1%; Score 31; DB 9; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QYQRESQA 11
Db 5 QYQHSQA 12

RESULT 8
US-09-853-253-25
; Sequence 25, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-25

Query Match      43.1%; Score 31; DB 9; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QYQRESQA 11
Db 5 QYQHSQA 12

RESULT 9
US-10-921-371-25
; Sequence 25, Application US/10921371
; Publication No. US20050048618A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/10/921,371
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US/09/853,253
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-921-371-25

Query Match      43.1%; Score 31; DB 17; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 QYQRESQA 11
Db 5 QYQHSQA 12
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; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLIMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022,066
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2002-09-09
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-938-68

Query Match      43.1%; Score 31; DB 15; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY  2 ITQYQRESQAYY 13
    |||:|:|
Db  1 IRDAQREDEAWY 12

RESULT 11
US-10-022-066-91
; Sequence 91, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLIMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022,066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-022-066-91

Query Match      41.7%; Score 30; DB 14; Length 18;
Best Local Similarity 40.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY  4 QYQRESQAYY 13
    ::|||:|:|
Db  7 RFMRNMSYY 16

RESULT 12
US-10-022-066-92
; Sequence 92, Application US/10022066
; Publication No. US20030166057A1
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; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLIMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022,066
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2002-09-09
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-022-066-92

Query Match      41.7%; Score 30; DB 14; Length 18;
Best Local Similarity 40.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY  4 QYQRESQAYY 13
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Db  7 RFMRNMSYY 16

RESULT 13
US-10-490-326-45
; Sequence 45, Application US/10490326
; Publication No. US20050070470A1
; GENERAL INFORMATION:
; APPLICANT: COY, David H.
; APPLICANT: FUSELIER, Joseph A.
; APPLICANT: MURPHY, William A.
; APPLICANT: SUN, Lichun
; TITLE OF INVENTION: Diagnostic or Therapeutic Somatostatin or
; FILE OF INVENTION: Bombesin Analog Conjugates and Uses Thereof
; FILE REFERENCE: 07005/005002
; CURRENT APPLICATION NUMBER: US/10/490,326
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: PCT/US02/30143
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/323,851
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 14..19
; OTHER INFORMATION: Cys at positions 14 and 19 are circularized
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-490-326-45

Query Match      41.7%; Score 30; DB 17; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY  4 QYQRESQAYY 13
    |||:|:|
Db  4 QQQQQQQQY 13
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RESULT 14
 US-10-192-869-7
 ; Sequence 7, Application US/10192869
 ; Publication No. US2003022265A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Park, Woo-Jim
 ; APPLICANT: Kim, Sung-Yun
 ; APPLICANT: Park, Dae-Ho
 ; TITLE OF INVENTION: Method for Determining Substrate Specificity of Protease
 ; FILE REFERENCE: HYLE68.001AUS
 ; CURRENT APPLICATION NUMBER: US/10/192,869
 ; CURRENT FILING DATE: 2002-07-08
 ; PRIOR APPLICATION NUMBER: KR 10-2001-0041011
 ; PRIOR FILING DATE: 2001-07-09
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: Fast-SEQ 4.0
 ; SEQ ID NO 7
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial Peptide substrate for kex2
 US-10-192-869-7

Query Match 38.9%; Score 28; DB 14; Length 10;
 Best Local Similarity 40.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 ITOYQRESQA 11
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 Db 1 VMYRREAE 10

RESULT 15
 US-10-195-730-375
 ; Sequence 375, Application US/10195730
 ; Publication No. US2003014492A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et. al
 ; TITLE OF INVENTION: 101 Human Secreted Proteins
 ; FILE REFERENCE: P2017P1
 ; CURRENT APPLICATION NUMBER: US/10/195,730
 ; CURRENT FILING DATE: 2002-07-16
 ; PRIOR APPLICATION NUMBER: US/09/281,976
 ; PRIOR FILING DATE: 1999-03-31
 ; PRIOR APPLICATION NUMBER: 60/060,837
 ; PRIOR FILING DATE: 1997-10-02
 ; PRIOR APPLICATION NUMBER: 60/060,862
 ; PRIOR FILING DATE: 1997-10-02
 ; NUMBER OF SEQ ID NOS: 390
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 375
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-195-730-375

Query Match 38.9%; Score 28; DB 14; Length 17;
 Best Local Similarity 62.5%; Pred. No. 6.5e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CITOYORE 8
 : |::|:
 Db 3 CLTQLRE 10

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 Job time : 220.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2005, 15:38:13 ; Search time 219.5 Seconds
(without alignments)
23.982 Million cell updates/sec

Title: US-09-576-724-1

Perfect score: 72

Sequence: 1 CITOYERESQAYY 13

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Gapop 10.0 , Gapext 0.5

Searched: 1812044 seqs, 404927589 residues

Total number of hits satisfying chosen parameters: 361688

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

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3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	69	95.8	15	14	US-10-116-061-48
2	69	95.8	19	15	US-10-614-370-4
3	69	95.8	19	18	US-10-508-296-8
4	40	55.6	12	9	US-09-791-378-590
5	40	55.6	12	11	US-09-791-377-590
6	30	41.7	18	18	US-10-938-992-24
7	30	41.7	18	18	US-10-938-992-50
8	29	40.3	18	14	US-10-022-066-87
9	29	40.3	20	17	US-10-690-276-453
10	28	38.9	9	17	US-10-621-675-320
11	28	38.9	13	9	US-09-853-253-26
					Sequence 48, Appl
					Sequence 4, Appl
					Sequence 8, Appl
					Sequence 590, App
					Sequence 24, Appl
					Sequence 50, Appl
					Sequence 87, Appl
					Sequence 453, App
					Sequence 320, App
					Sequence 26, Appl

12	38.9	13	17	US-10-921-371-26	Sequence 26, Appl
13	38.9	15	9	US-09-853-253-25	Sequence 25, Appl
14	38.9	15	14	US-10-347-562-13	Sequence 13, Appl
15	38.9	15	14	US-10-351-641-1553	Sequence 1553, App
16	38.9	15	17	US-10-921-371-25	Sequence 25, Appl
17	38.9	17	15	US-10-403-938-68	Sequence 68, Appl
18	38.9	18	14	US-10-022-066-91	Sequence 91, Appl
19	38.9	18	14	US-10-022-066-92	Sequence 92, Appl
20	38.9	18	15	US-10-227-012-2	Sequence 2, Appl
21	38.9	18	17	US-10-808-187-840	Sequence 840, App
22	38.9	18	18	US-10-807-807-840	Sequence 840, App
23	38.9	20	16	US-10-776-013-255	Sequence 255, App
24	38.9	20	16	US-10-776-013-255	Sequence 255, App
25	37.5	9	17	US-10-621-675-319	Sequence 319, App
26	37.5	10	14	US-10-192-869-7	Sequence 7, Appl
27	37.5	14	16	US-10-807-837-60	Sequence 60, Appl
28	37.5	15	15	US-10-634-262-28	Sequence 28, Appl
29	37.5	15	16	US-10-732-345-2	Sequence 2, Appl
30	37.5	17	14	US-10-225-322-4	Sequence 4, Appl
31	37.5	17	14	US-10-195-730-375	Sequence 375, App
32	37.5	17	15	US-10-609-217-430	Sequence 430, App
33	37.5	17	15	US-10-632-388-430	Sequence 430, App
34	37.5	17	15	US-10-651-723-430	Sequence 430, App
35	37.5	17	15	US-10-645-761-430	Sequence 430, App
36	37.5	17	15	US-10-666-696-430	Sequence 430, App
37	37.5	17	15	US-10-653-048-430	Sequence 430, App
38	37.5	17	16	US-10-799-747-375	Sequence 375, App
39	37.5	17	16	US-10-821-544-10	Sequence 10, Appl
40	37.5	17	16	US-10-821-544-12	Sequence 12, Appl
41	37.5	17	17	US-10-979-183-375	Sequence 375, App
42	37.5	17	18	US-10-645-784-430	Sequence 430, App
43	37.5	18	15	US-10-609-217-903	Sequence 903, App
44	37.5	18	15	US-10-632-388-903	Sequence 903, App
45	37.5	18	15	US-10-651-723-903	Sequence 903, App

ALIGNMENTS

RESULT 1
US-10-116-061-48
; Sequence 48, Application US/10116061
; Publication No. US20030199013A1
; GENERAL INFORMATION:
; APPLICANT: Fishleigh, Robert V.
; Meese, Roger P.
; TITLE OF INVENTION: Fragments of Prion Proteins
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/116,061
; FILING DATE: 05-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,701B
; FILING DATE: 02-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Panucci, Allan A.
; REGISTRATION NUMBER: 30,256
; REFERENCE/DOCKET NUMBER: 8080-007
; TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-116-061-48

Query Match          95.8%; Score 69; DB 14; Length 15;
Best Local Similarity 92.3%; Pred. No. 3e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYERESQAYY 13
   |||||:|||||
Db 1 CITQYERESQAYY 13

RESULT 2
US-10-614-370-4
; Sequence 4, Application US/10614370
; Publication No. US20040091474A1
; GENERAL INFORMATION:
; APPLICANT: Raven, Neil David Hammond
; TITLE OF INVENTION: Degradation and Detection of TSE Infectivity
; FILE REFERENCE: 1581.0990001
; CURRENT APPLICATION NUMBER: US/10/614,370
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: GB 0104696.0
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: GB 0100420.9
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: GB 0216146.1
; PRIOR FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: PCT/GB02/00052
; PRIOR FILING DATE: 2002-01-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-614-370-4

Query Match          95.8%; Score 69; DB 15; Length 19;
Best Local Similarity 92.3%; Pred. No. 3.9e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYERESQAYY 13
   |||||:|||||
Db 1 CITQYERESQAYY 13

RESULT 3
US-10-508-296-8
; Sequence 8, Application US/10508296
; Publication No. US20050163776A1
; GENERAL INFORMATION:
; APPLICANT: Microbiological Research Authority
; APPLICANT: Raven, Neil
; APPLICANT: Sutton, John
; APPLICANT: Murdoch, Heather
; TITLE OF INVENTION: Treatment of TSE Infection
; FILE REFERENCE: GWS/GMS/24416WQ
; CURRENT APPLICATION NUMBER: US/10/508,296
; CURRENT FILING DATE: 2004-09-20

; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-116-061-48

Query Match          95.8%; Score 69; DB 14; Length 15;
Best Local Similarity 92.3%; Pred. No. 3e-05;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYERESQAYY 13
   |||||:|||||
Db 1 CITQYERESQAYY 13

RESULT 4
US-09-791-378-590
; Sequence 590, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 590
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Synthetic
US-09-791-378-590

Query Match          55.6%; Score 40; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYER 7
   |||||
Db 6 CITQYER 12

RESULT 5
US-09-791-377-590
; Sequence 590, Application US/09791377
; Publication No. US20040110938A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 9195-060-999
; CURRENT APPLICATION NUMBER: US/09/791,377
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 590
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Synthetic
US-09-791-377-590
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Query Match 55.6%; Score 40; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITOYER 7
DB 6 CITOYER 12

RESULT 6
US-10-938-992-24
; Sequence 24, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; APPLICANT: Qin, Shixin
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Obar, Robert
; TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
; FILE REFERENCE: 3258.1033-001
; CURRENT APPLICATION NUMBER: US/10/938,992
; PRIOR FILING DATE: 2004-09-10
; PRIOR FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-992-24

Query Match 41.7%; Score 30; DB 18; Length 18;
Best Local Similarity 55.6%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 QYERESQAY 12
DB 10 RYEREMKY 18

RESULT 7
US-10-938-992-50
; Sequence 50, Application US/10938992
; Publication No. US20050152903A1
; GENERAL INFORMATION:
; APPLICANT: Newman, Walter
; APPLICANT: Qin, Shixin
; APPLICANT: O'Keefe, Theresa
; APPLICANT: Obar, Robert
; TITLE OF INVENTION: Monoclonal Antibodies Against HMGB1
; FILE REFERENCE: 3258.1033-001
; CURRENT APPLICATION NUMBER: US/10/938,992
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: 60/502,568
; PRIOR FILING DATE: 2003-09-11
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-992-50

Query Match 41.7%; Score 30; DB 18; Length 18;
Best Local Similarity 55.6%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 QYERESQAY 12
DB 4 RYEREMKY 12

RESULT 8
US-10-022-066-87
; Sequence 87, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLIMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022,066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-022-066-87

Query Match 40.3%; Score 29; DB 14; Length 18;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 QYERESQAY 13
DB 7 RPEREISNY 16

RESULT 9
US-10-690-276-453
; Sequence 453, Application US/10690276
; Publication No. US20050112118A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Incorporated
; APPLICANT: Cimbora, Daniel
; APPLICANT: Heichman, Karen
; APPLICANT: Bartel, Paul
; APPLICANT: Mauck, Kimberly
; APPLICANT: Bush, Angie
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING INFLAMMATORY DISORDERS
; FILE REFERENCE: 1834.01
; CURRENT APPLICATION NUMBER: US/10/690,276
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: 09/727,384
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 60/168,377
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: 60/168,379
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: 60/185,056
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 10/035,344
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,571
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 10/035,343
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,572
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 10/099,924
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,179
; PRIOR FILING DATE: 2001-03-15

; Remaining Prior Application data removed - See File Wrapper or PALM.

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; NUMBER OF SEQ ID NOS: 728
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 453
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-690-276-453

Query Match          40.3%; Score 29; DB 17; Length 20;
Best Local Similarity 44.4%; Pred. No. 5.2e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      5 YERESQAYY 13
DB      10 YERNGEVFY 18

RESULT 10
US-10-621-675-320
; Sequence 320, Application US/10621675
; Publication No. US20050049398A1
; GENERAL INFORMATION:
; APPLICANT: De Leys, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; TITLE OF INVENTION: CONTAINING THEM
; FILE REFERENCE: 2752-11
; CURRENT APPLICATION NUMBER: US/10/621,675
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US/09/576,824A
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 08/723,425
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 320
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-621-675-320

Query Match          38.9%; Score 28; DB 17; Length 9;
Best Local Similarity 55.8%; Pred. No. 1.6e+06;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2 ITQYERESQ 10
DB      1 ITRYSEKN 9

RESULT 11
US-09-853-253-26
; Sequence 26, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: (13)...(13)
US-09-853-253-26

Query Match          38.9%; Score 28; DB 9; Length 13;
Best Local Similarity 62.5%; Pred. No. 4.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 QYERESQA 11
DB      5 QYQHSQA 12

RESULT 12
US-10-921-371-26
; Sequence 26, Application US/10921371
; Publication No. US20050048618A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/10/921,371
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: US/09/853,253
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: AMIDATION
; LOCATION: (13)...(13)
US-10-921-371-26

Query Match          38.9%; Score 28; DB 17; Length 13;
Best Local Similarity 62.5%; Pred. No. 4.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 QYERESQA 11
DB      5 QYQHSQA 12

RESULT 13
US-09-853-253-25
; Sequence 25, Application US/09853253
; Patent No. US20020055156A1
; GENERAL INFORMATION:
; APPLICANT: JASPERS, STEPHEN
; APPLICANT: SHEPPARD, PAUL
; APPLICANT: DEISHER, THERESA
; APPLICANT: BISHOP, PAUL
; TITLE OF INVENTION: Zsig33-like Peptides
; FILE REFERENCE: 00-30
; CURRENT APPLICATION NUMBER: US/09/853,253
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,300
; PRIOR FILING DATE: 2000-05-11
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; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-253-25

Query Match 38.9%; Score 28; DB 9; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 QYERESQA 11
|::|||
DB 5 QYQHSQA 12

RESULT 14

US-10-347-562-13
; Sequence 13, Application US/10347562
; Publication No. US2003016555A1
; GENERAL INFORMATION:
; APPLICANT: Ding, S.
; APPLICANT: Kang, M. T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ADMINISTRATION OF
; TITLE OF INVENTION: THERAPEUTIC REAGENTS
; FILE REFERENCE: 7872-104
; CURRENT APPLICATION NUMBER: US/10/347,562
; CURRENT FILING DATE: 2003-01-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: enhancer peptide
US-10-347-562-13

Query Match 38.9%; Score 28; DB 14; Length 15;
Best Local Similarity 55.6%; Pred. No. 5.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 QYERESQA 12
|::|||
DB 3 EWEREISAY 11

RESULT 15

US-10-351-641-1553
; Sequence 1553, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1553

; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1553

Query Match 38.9%; Score 28; DB 14; Length 15;
Best Local Similarity 55.6%; Pred. No. 5.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 QYERESQA 12
|::|||
DB 3 EWEREISAY 11

Search completed: September 15, 2005, 16:13:05
Job time : 233.5 secs

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OM protein - protein search, using sw model

Run on: September 15, 2005, 15:23:47 ; Search time 37 Seconds
(without alignments)
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Title: US-09-576-724-1

Perfect score: 72
Sequence: 1 CITQYERESQAYY 13

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 196327

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Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	69	95.8	17	3	US-09-353-348-3
5	34	47.2	16	3	US-08-916-246-5
6	34	47.2	16	4	US-09-949-186-5
7	32	44.4	14	2	US-08-750-856A-11
8	30	41.7	12	6	5210075-22
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10	29	40.3	20	2	US-08-637-759B-459
11	29	40.3	20	3	US-08-871-355A-459
12	29	40.3	20	3	US-09-201-945-459
13	28	38.9	6	3	US-09-353-348-1
14	28	38.9	9	2	US-08-146-028-372
15	28	38.9	9	3	US-08-723-425A-372
16	28	38.9	9	4	US-09-112-206-372
17	28	38.9	9	4	US-09-790-497A-320
18	28	38.9	9	4	US-09-576-824A-320
19	28	38.9	9	4	US-09-680-497-372
20	28	38.9	15	3	US-09-315-304B-1553
21	28	38.9	15	4	US-09-350-325-13
22	28	38.9	15	4	US-09-350-641C-1553
23	27	37.5	9	2	US-08-146-028-371
24	27	37.5	9	3	US-08-723-425A-371
25	27	37.5	9	3	US-09-112-206-371
26	27	37.5	9	4	US-09-790-497A-319
27	27	37.5	9	4	US-09-576-824A-319

Sequence 371, App
Sequence 313, App
Sequence 333, App
Sequence 311, App
Sequence 331, App
Sequence 26, Appli
Sequence 335, App
Sequence 2, Appli
Sequence 28, Appli
Sequence 4, Appli
Sequence 430, App
Sequence 10, Appl
Sequence 12, Appl
Sequence 312, App
Sequence 332, App
Sequence 330, App
Sequence 333, App
Sequence 903, App

28 27 37.5 9 4 US-09-680-497-371
29 27 37.5 14 1 US-08-465-391A-313
30 27 37.5 14 1 US-08-465-391A-313
31 27 37.5 14 2 US-08-464-538B-311
32 27 37.5 14 2 US-08-464-538B-311
33 27 37.5 14 2 US-08-463-076B-26
34 27 37.5 14 2 US-08-463-076B-335
35 27 37.5 15 4 US-09-947-372A-2
36 27 37.5 15 4 US-09-554-467A-28
37 27 37.5 17 4 US-09-459-958-4
38 27 37.5 17 4 US-09-428-082B-430
39 27 37.5 17 4 US-09-155-260C-10
40 27 37.5 17 4 US-09-155-260C-12
41 27 37.5 18 1 US-08-383-474B-312
42 27 37.5 18 1 US-08-465-391A-312
43 27 37.5 18 2 US-08-464-538B-330
44 27 37.5 18 2 US-08-463-076B-333
45 27 37.5 18 4 US-09-428-082B-903

ALIGNMENTS

RESULT 1

US-09-380-015B-9

; Sequence 9, Application US/09380015B

; Patent No. 6765088

; GENERAL INFORMATION:

; APPLICANT: Carsten Korth

; TITLE OF INVENTION: Immunological Detection of Prions

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kanton Zuerich vertreten durch die Erziehungsdirektion

; STREET: Walcheter

; CITY: Zuerich

; STATE: Zuerich

; COUNTRY: Switzerland

; ZIP: CH-8090

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/380,015B

; FILING DATE: 23-Aug-1999

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 97102837.8

; FILING DATE: 21-FEB-1997

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: YES

; ANTI-SENSE: NO

; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-380-015B-9

Query Match

Best Local Similarity 95.8%; Score 69; DB 4; Length 13;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CITQYERESQAYY 13

Db 1 CITQYERESQAYY 13

RESULT 2

US-08-244-701B-48

; Sequence 48, Application US/08244701B

; Patent No. 5773572
; GENERAL INFORMATION:
; APPLICANT: Fishleigh, Robert V.
; APPLICANT: Robson, Barry
; APPLICANT: Mee, Roger P.
; TITLE OF INVENTION: Fragments of Prion Proteins
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,701B
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Fanucci, Allan A.
; REGISTRATION NUMBER: 30,256
; REFERENCE/DOCKET NUMBER: 8080-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-244-701B-48

Query Match 95.8%; Score 69; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 2.9e-06;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYERESQAYY 13
| | | | | | | | | | | | | | |
Db 1 CITQYERESQAYY 13

RESULT 3
US-09-076-721-48
; Sequence 48, Application US/09076721
; Patent No. 6373905
; GENERAL INFORMATION:
; APPLICANT: Fishleigh, Robert V.
; APPLICANT: Robson, Barry
; APPLICANT: Mee, Roger P.
; TITLE OF INVENTION: Fragments of Prion Proteins
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/076,721

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/244,701
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fanucci, Allan A.
; REGISTRATION NUMBER: 30,256
; REFERENCE/DOCKET NUMBER: 8080-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-076-721-48

Query Match 95.8%; Score 69; DB 3; Length 15;
Best Local Similarity 92.3%; Pred. No. 2.9e-06;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYERESQAYY 13
| | | | | | | | | | | | | | |
Db 1 CITQYERESQAYY 13

RESULT 4
US-09-353-348-3
; Sequence 3, Application US/09353348
; Patent No. 6261790
; GENERAL INFORMATION:
; APPLICANT: O'Rourke, Katherine I.
; TITLE OF INVENTION: Monoclonal Antibodies and Antibody Cocktail for
; TITLE OF INVENTION: Detection of Prion Protein as an Indication of
; TITLE OF INVENTION: Transmissible Spongiform Encephalopathies
; FILE REFERENCE: O'Rourke
; CURRENT APPLICATION NUMBER: US/09/353,348
; CURRENT FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Ovis aries
US-09-353-348-3

Query Match 95.8%; Score 69; DB 3; Length 17;
Best Local Similarity 92.3%; Pred. No. 3.3e-06;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQYERESQAYY 13
| | | | | | | | | | | | | | |
Db 1 CITQYERESQAYY 13

RESULT 5
US-08-916-246-5
; Sequence 5, Application US/08916246
; Patent No. 6323020
; GENERAL INFORMATION:
; APPLICANT: Perryman, Lance E.
; APPLICANT: Jasmer, Douglas P.
; APPLICANT: Riggs, Michael W.
; APPLICANT: McGuire, Travis C.
; TITLE OF INVENTION: NEUTRALIZATION-SENSITIVE EPITOPES OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Kenneth Sibley, Myers Bigel Sibley & Sajovec
STREET: PO BOX 37428
CITY: Raleigh
STATE: No. 6323020th Carolina
COUNTRY: USA
ZIP: 27627
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,246
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051-405
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1400
TELEFAX: 919-854-1401
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-916-246-5

Query Match 47.2%; Score 34; DB 3; Length 16;
Best Local Similarity 85.7%; Pred. No. 8.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 RESQAYY 13
:|||||
Db 1 KESQAYY 7

RESULT 6
US-09-949-186-5
Sequence 5, Application US/09949186
Patent No. 6759048
GENERAL INFORMATION:
APPLICANT: Perryman, Lance E
APPLICANT: Jasmer, Douglas P.
APPLICANT: Riggs, Michael W.
APPLICANT: McGuire, Travis C.
TITLE OF INVENTION: NEUTRALIZATION-SENSITIVE EPITOPES OF CRYPTOSPORIDIUM PARVUM
FILE REFERENCE: 5051.405DV
CURRENT APPLICATION NUMBER: US/09/949,186
CURRENT FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-09-949-186-5

Query Match 47.2%; Score 34; DB 4; Length 16;
Best Local Similarity 85.7%; Pred. No. 8.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 RESQAYY 13
:|||||
Db 1 KESQAYY 7

RESULT 7

US-08-750-856A-11
Sequence 11, Application US/08750856A
Patent No. 5858672
GENERAL INFORMATION:
APPLICANT: SONIGO, PIERRE
APPLICANT: PANCINO, GIANFRANCO
APPLICANT: PETERHANS, ERNST
APPLICANT: BERTONI, GIUSEPPE
TITLE OF INVENTION: NUCLEIC ACID FRAGMENTS AND CORRESPONDING
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,856A
FILING DATE: 30-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/07933
FILING DATE: 28-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 917-052-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-750-856A-11

Query Match 44.4%; Score 32; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 QVERESQAY 12
:|||||
Db 5 QWERELQY 13

RESULT 8
5210075-22
Patent No. 5210075
APPLICANT: SCHOLTZ, WOLFGANG;CHIANG, SHIU-LANG;NAGARAJAN,
GOBILOBL, THOMAS J.
TITLE OF INVENTION: INTERLEUKIN 6 ANTAGONIST PEPTIDES
NUMBER OF SEQUENCES: 69
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,868
FILING DATE: 16-FEB-1990
SEQ ID NO:22:
LENGTH: 12
5210075-22

Query Match 41.7%; Score 30; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 32;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 TOYRESQAY 12
:||:|:|:|:
Db 3 SQYSQESQLF 12

RESULT 9
US-08-637-759B-459
; Patent No. 5210075
; APPLICANT: SCHOLTZ, WOLFGANG; CHIANG, SHIU-LANG; NAGARAJAN,
; GOBI; LOBL, THOMAS J.
; TITLE OF INVENTION: INTERLEUKIN 6 ANTAGONIST PEPTIDES
; NUMBER OF SEQUENCES: 69
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,868
; FILING DATE: 16-FEB-1990
; SEQ ID NO: 22:
; LENGTH: 12
5210075-22

Query Match 41.7%; Score 30; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 TOYRESQAY 12
:||:|:|:|:
Db 3 SQYSQESQLF 12

RESULT 10
US-08-637-759B-459
; Sequence 459, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,759B
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 459:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; HYPOTHETICAL: NO
US-08-637-759B-459

Query Match 40.3%; Score 29; DB 2; Length 20;
Best Local Similarity 55.6%; Pred. No. 88;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 YERESQAY 13
:||:|:|:|:
Db 7 YERENRTAY 15

RESULT 11
US-08-871-355A-459
; Sequence 459, Application US/08871355A
; Patent No. 6015669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,355A
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 459:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-871-355A-459

Query Match 40.3%; Score 29; DB 3; Length 20;
Best Local Similarity 55.6%; Pred. No. 88;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 YERESQAY 13
:||:|:|:|:
Db 7 YERENRTAY 15

RESULT 12
US-09-201-945-459
; Sequence 459, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
; APPLICANT: David William Holden

;; TITLE OF INVENTION: Identification of Genes
;; NUMBER OF SEQUENCES: 501
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Patrea L. Pabst
;; STREET: 2800 One Atlantic Center
;; STREET: 1201 West Peachtree Street
;; CITY: Atlanta
;; STATE: Georgia
;; COUNTRY: USA
;; ZIP: 30309-3450
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/201,945
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/637,759
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pabst, Patrea L.
;; REGISTRATION NUMBER: 31,284
;; REFERENCE/DOCKET NUMBER: RPMS 101
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (404) 873-8794
;; TELEFAX: (404) 873-8795
;; INFORMATION FOR SEQ ID NO: 459:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; US-09-201-945-459

Query Match 40.3%; Score 29; DB 3; Length 20;
Best Local Similarity 55.6%; Pred. No. 88;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 YERESQAY 13
|||:|
Db 7 YERENTAY 15

RESULT 13
US-09-353-348-1
; Sequence 1, Application US/09353348
; Patent No. 6261790
; GENERAL INFORMATION:
; APPLICANT: O'Rourke, Katherine I.
; TITLE OF INVENTION: Monoclonal Antibodies and Antibody Cocktail for
; TITLE OF INVENTION: Detection of Prion protein as an indication of
; TITLE OF INVENTION: Transmissible Spongiform Encephalopathies
; FILE REFERENCE: O'Rourke
; CURRENT APPLICATION NUMBER: US/09/353,348
; CURRENT FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Ovis aries
US-09-353-348-1

Query Match 38.9%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.1e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 QYERES 9
|||:|
Db 1 QYQRES 6

RESULT 14
US-08-146-028-372
; Sequence 372, Application US/08146028
; Patent No. 5891640
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,028
; INFORMATION FOR SEQ ID NO: 372:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-146-028-372

Query Match 38.9%; Score 28; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ITQYERESQ 10
|||:|
Db 1 ITRYESENK 9

RESULT 15
US-08-723-425A-372
; Sequence 372, Application US/08723425A
; Patent No. 6165730
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
; NUMBER OF SEQUENCES: 453
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE, P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723,425A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-13

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 372:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-723-425A-372

Query Match 38.9%; Score 28; DB 3; Length 9;
Best Local Similarity 55.6%; Pred. No. 4.1e+05;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ITOYERESQ 10
Db 1 ITRYSENK 9

Search completed: September 15, 2005, 15:50:31
Job time : 41 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension **.rnp**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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OM protein - protein search, using sw model

Run on: September 15, 2005, 15:50:48 ; Search time 621 Seconds
(without alignments)
10.720 Million cell updates/sec

Title: US-09-576-724-1
Perfect score: 72
Sequence: 1 CITQYERESQAYY 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 12050

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	36.1	13	2 Q8WFR5	Q8wfr5 diadema pau
2	25	34.7	8	2 Q718T2	Q718t2 newcastie d
3	24	33.3	9	2 Q7RSP2	Q7rsp2 plasmodium
4	24	33.3	18	2 Q7RNN4	Q7rnn4 plasmodium
5	24	33.3	20	2 Q9S878	Q9s878 petunia hyb
6	24	33.3	20	2 Q93TW0	Q93tw0 neisseria m
7	23	31.9	13	2 Q936V1	Q936v1 pseudomonas
8	23	31.9	15	1 UC16 MAIZE	P80622 zea mays (m
9	23	31.9	15	2 Q7KQF8	Q7kqf8 drosophila
10	23	31.9	17	2 Q8J167	Q8j167 trichoderma
11	22	30.6	10	2 Q9QVE7	Q9qve7 mus sp. pro
12	22	30.6	10	2 Q9QVE8	Q9qve8 mus sp. pro
13	22	30.6	11	2 P97755	P97755 rattus norv
14	22	30.6	14	2 Q85CA1	Q85ca1 strongyloce
15	22	30.6	15	2 Q6SLH8	Q6slh8 caenorhabdi
16	22	30.6	15	2 Q7MOK8	Q7mok8 corynebacte
17	22	30.6	17	2 Q9V2X3	Q9v2x3 methanobact
18	22	30.6	17	2 Q9PS12	Q9ps12 gallus gall
19	21	29.2	8	2 Q95M23	Q95m23 sus scrofa
20	21	29.2	13	1 NEUT CAVPO	P32560 cavia porce
21	21	29.2	14	2 Q8LIY9	Q8liy9 chroococcid
22	21	29.2	15	1 UC14 MAIZE	P80620 zea mays (m
23	21	29.2	16	1 LEC_DELRE	P83511 delonix reg
24	21	29.2	16	2 Q9TRM5	Q9trm5 bos taurus
25	21	29.2	17	2 Q06800	Q06800 saccharomyc
26	21	29.2	18	2 Q7SB67	Q7sb67 neurospora
27	21	29.2	18	2 Q936D0	Q936d0 staphylococ
28	21	29.2	19	2 Q85AZ5	Q85az5 arapauna gi
29	21	29.2	19	2 Q85RP4	Q85rp4 arapauna gi
30	21	29.2	20	2 Q6E807	Q6e807 ovis aries
31	21	29.2	20	2 Q64FZ8	Q64fz8 pisum sativ

32	21	29.2	20	2 Q8CJD7	Q8cjd7 rattus norv
33	21	29.2	20	2 Q9PRM4	Q9prm4 gallus gall
34	20	27.8	9	2 Q6VFO2	Q6vfg2 vibrio fisc
35	20	27.8	11	2 Q800X7	Q800x7 chelydra se
36	20	27.8	13	2 Q16141	Q16141 homo sapien
37	20	27.8	14	2 P82209	P82209 bombyx mori
38	20	27.8	14	2 Q7M2L3	Q7m2l3 bos taurus
39	20	27.8	15	2 Q9TR89	Q9tr89 bos taurus
40	20	27.8	15	2 Q9TRP1	Q9trp1 sus scrofa
41	20	27.8	16	2 Q9UP51	Q9up51 homo sapien
42	20	27.8	17	1 GAST MACMU	P33714 macaca mula
43	20	27.8	17	2 Q94758	Q94758 sclerotinia
44	20	27.8	17	2 Q8J168	Q8j168 trichoderma
45	20	27.8	17	2 Q8NIJ6	Q8nij6 fusarium so

ALIGNMENTS

RESULT 1					
Q8WFR5 PRELIMINARY; PRT; 8 AA.					
AC	Q8WFR5	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)				
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)				
DE	Cytochrome oxidase subunit II (Fragment).				
GN	Name=COII;				
OS	Diadema paucispinum.				
OG	Mitochondrion.				
OC	Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;				
OC	Echinoidea; Euechinoidea; Diadematacea; Diadematoidea; Diadematiidae;				
OC	Diadema.				
OX	NCBI_TaxID=145530;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21323357; PubMed=11430656;				
RA	Lessios H.A., Kessing B.D., Pearse J.S.;				
RT	"Population structure and speciation in tropical seas: global				
RT	phylogeography of the sea urchin Diadema.";				
RL	Evolution 55:955-975(2001).				
DR	EMBL; AY012959; AAL33852.1; -				
DR	GO; GO:0005739; C:mitochondrion; IEA.				
KW	Mitochondrion.				
FT	NON TER				
SQ	SEQUENCE 8 AA; 954 MW; C41B173B46DDC2CE CRC64;				

Query Match 36.1%; Score 26; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. NO. 1.6e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CITQYERE 8
|: |||
Db 1 CVAQYLEE 8

RESULT 2					
Q718T2 PRELIMINARY; PRT; 13 AA.					
AC	Q718T2	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)				
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)				
DE	Hemagglutinin-neuraminidase (Fragment).				
OS	Newcastle disease virus.				
OC	Viruses; SSRNA negative-strand viruses; Mononegavirales;				
OC	Paramyxoviridae; Paramyxovirinae; Avulavirus.				
OX	NCBI_TaxID=11176;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Gould A.R., Hansson E., Selleck K., Kattenbelt J.A., Mackenzie M.,				
RA	Della-Porta A.J.;				
RT	"Newcastle disease virus fusion and hemagglutinin-neuraminidase gene				

```

RT motifs as markers for viral lineage.";
RL Avian Pathol. 32:361-373(2003).
DR EMBL; AF542841; AAQ11566.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1628 MW; 685A336009B645BB CRC64;

Query Match 34.7%; Score 25; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 9e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 YERESQAY 12
Db ||| |
1 YRELESY 8

RESULT 3
Q7RSP2 Q7RSP2 PRELIMINARY; PRT; 9 AA.
AC Q7RSP2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Names=PY00313;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01000480; EAA21149.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2241 MW; 1D1B621B9CB920AE CRC64;

Query Match 33.3%; Score 24; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 RESQAY 12
Db ||| |
2 RESQFY 7

RESULT 5
Q9S878 Q9S878 PRELIMINARY; PRT; 20 AA.
AC Q9S878;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADPH-cytochrome P450 reductase (EC 1.6.2.4) (Fragment).
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE.
RX MEDLINE=95083756; PubMed=7991686; DOI=10.1104/pp.106.2.643;
RA Menting J.G., Cornish E., Scopes R.K.;
RT "Purification and partial characterization of NADPH-cytochrome c
RT reductase from Petunia hybrida flowers.";
RL Plant Physiol. 106:643-650(1994).
DR GO; GO:0003958; F:NADPH-hemoprotein reductase activity; IEA.
SQ SEQUENCE 20 AA; 2390 MW; 8BCDA6F8CF7EEDE CRC64;

Query Match 33.3%; Score 24; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 YERESQAY 12
Db ||| |
6 YEEELQSF 13

RESULT 6
Q93TWO Q93TWO PRELIMINARY; PRT; 20 AA.
AC Q93TWO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fillin glycosylation protein Pgic (Fragment).

```

0:

```
Db      | : : | | |
        6 OQQAQSGGY 15

RESULT 10
Q8J167  PRELIMINARY;      PRT;      17 AA.
AC Q8J167;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Translation elongation factor (fragment).
GN Name=TEF;
OS Trichoderma harzianum (Hypocrea lixii).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
OX NCBI_TaxID=5544;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GJS 98-6;
RX MEDLINE=22582157; PubMed=12695093; DOI=10.1016/S1055-7903(02)00400-1;
RA Chaverri P., Castlebury L.A., Samuels G.J., Geiser D.M.;
RT "Multilocus phylogenetic structure within the Trichoderma
harzianum/Hypocrea lixii complex.";
RL Mol. Phylogenet. Evol. 27:302-313(2003).
DR EMBL; AF469195; AAC14641.1; -.
DR GO; GO:0003746; F:translation elongation factor activity; IEA.
KW Elongation factor.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2020 MW; 017BAFF1817FF1C6 CRC64;

Query Match 31.9%; Score 23; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ITQVERES 9
| : : | |
Db 1 IEKFEKES 8

RESULT 11
Q9QVE7  PRELIMINARY;      PRT;      10 AA.
AC Q9QVE7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Protamine MP2 intermediate protein PMP2/20 (fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=92174934; PubMed=1541289;
RA Chauviere M., Martinage A., Debarle M., Sautiere P., Chevaillier P.;
RT "Molecular characterization of six intermediate proteins in the
processing of mouse protamine P2 precursor.";
RL Eur. J. Biochem. 204:759-765(1992).
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1197 MW; 79920ED866DB1B04 CRC64;

Query Match 30.6%; Score 22; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 YERESQ 10
| : : | |
Db 1 HEREEQ 6

RESULT 12
Q9QVE8  PRELIMINARY;      PRT;      10 AA.
AC Q9QVE8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Protamine MP2 intermediate protein PMP2/16 (fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=92174934; PubMed=1541289;
RA Chauviere M., Martinage A., Debarle M., Sautiere P., Chevaillier P.;
RT "Molecular characterization of six intermediate proteins in the
processing of mouse protamine P2 precursor.";
RL Eur. J. Biochem. 204:759-765(1992).
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1224 MW; D4050B040B11EAB6 CRC64;

Query Match 30.6%; Score 22; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 YERESQ 10
| : : | |
Db 5 HEREEQ 10

RESULT 13
P97755  PRELIMINARY;      PRT;      11 AA.
AC P97755;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Secretogranin II (SGII) (fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96343805; PubMed=8756552; DOI=10.1210/en.137.9.3815;
RA Jones L.C., Day R.N., Pittler S.J., Valentine D.L., Scammell J.G.;
RT "Cell-specific expression of the rat secretogranin II promoter.";
RL Endocrinology 137:3815-3822(1996).
DR EMBL; AF107301; -; NOT_ANNOTATED_CDS.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1298 MW; 3E4E8DA446C1B5A7 CRC64;

Query Match 30.6%; Score 22; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 2.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 TOYERE 8
| : : | |
Db 6 TOYKTE 11

RESULT 14
Q85CA1  PRELIMINARY;      PRT;      14 AA.
AC Q85CA1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit II (fragment).
GN Name=COII;
OS Strongylocentrotus purpuratus (Purple sea urchin).
```


OG Mitochondrion.
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
 OC Strongylocentrotus.
 OX NCBI_TaxID=7668;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2207965; PubMed=12823452;
 RA Biermann C.H.; Kessing B.D.; Palumbi S.R.;
 RT "Phylogeny and development of marine model species: strongylocentrotid
 RL sea urchins";
 RL Evol. Dev. 5:360-371(2003).
 DR EMBL; AY221017; AAP21733.1; -
 DR EMBL; AY221018; AAP21736.1; -
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 1 1
 SQ SEQUENCE 14 AA; 1820 MW; 2CB850A51B616CD3 CRC64;

Query Match 30.6%; Score 22; DB 2; Length 14;
 Best Local Similarity 57.1%; Pred. No. 3.7e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OX 2 ITQYERE 8
 DE :||| |
 DE 8 VTQYLEE 14

RESULT 15
 Q6SLH8 PRELIMINARY; PRT; 15 AA.
 ID Q6SLH8
 AC Q6SLH8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE UORF2.
 GN Name=gna-2;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee M.-H.; Schedl T.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY455927; AAE26306.1; -
 SQ SEQUENCE 15 AA; 1901 MW; 86D1593BFA18C498 CRC64;

Query Match 30.6%; Score 22; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 4e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 6 ERESQAYY 13
 DB ||| :||
 DB 4 ERSFTSY 11

Search completed: September 15, 2005, 16:34:23
 Job time : 633.5 secs

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OM protein - protein search, using sw model

Run on: September 15, 2005, 16:05:21 ; Search time 24.5 Seconds
(without alignments)
51.054 Million cell updates/sec

Title: US-09-576-724-1

Perfect score: 72
Sequence: 1 CITQYERESQAY 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	33.3	18	2 B40741	T-cell receptor be
2	23	31.9	12	2 PH1605	Ig H chain V-D-J r
3	23	31.9	14	2 PT0252	Ig heavy chain CRD
4	23	31.9	14	2 E49039	T-cell receptor be
5	22	30.6	13	2 S47358	T-cell antigen rec
6	22	30.6	15	2 A17340	ribonucleoside-dip
7	21	29.2	13	2 A53608	neurotensin - guin
8	21	29.2	14	2 C40944	hypothetical prote
9	21	29.2	16	2 B44036	collagen alpha 1(X
10	21	29.2	20	2 PX0059	trypsin inhibitor
11	21	29.2	20	2 A47105	dystroglycan - chi
12	20	27.8	14	2 A39703	tubulin beta-3 cha
13	20	27.8	15	2 PH1613	Ig H chain V-D-J r
14	20	27.8	17	1 GMSH	gastrin - sheep
15	20	27.8	17	2 A60071	gastrin - rhesus m
16	20	27.8	18	2 JP0102	fibrinogen beta ch
17	20	27.8	19	2 PH1609	Ig H chain V-D-J r
18	19.5	27.1	19	2 A49254	TCR delta chain V-
19	19	26.4	10	2 C54226	light-harvesting p
20	19	26.4	13	2 S12388	arga protein - Sal
21	19	26.4	13	2 S47381	T-cell antigen rec
22	19	26.4	13	2 S14316	photosystem I 9K c
23	19	26.4	14	2 PT0232	Ig heavy chain CRD
24	19	26.4	14	2 S57569	T cell receptor V-
25	19	26.4	14	2 PH1597	Ig H chain V-D-J r
26	19	26.4	14	2 PH1471	T-cell receptor be
27	19	26.4	14	2 PC7079	unidentified 27.2K
28	19	26.4	15	2 PA0057	adenylate isopente
29	19	26.4	15	2 S36893	ribosomal protein

30 19 26.4 15 2 PA0062 fumarate hydratase
31 19 26.4 16 2 A44823 synaptosomal-aesoc
32 19 26.4 17 2 I67526 CD33 antigen homol
33 19 26.4 18 2 PQ0022 fixa protein - Rhi
34 19 26.4 18 2 A43334 orfl 5' of aadr -
35 19 26.4 18 2 S54270 GATA-2 protein - A
36 19 26.4 20 2 S06150 photosystem I chai
37 19 26.4 20 2 S27351 lysophospholipase
38 19 26.4 20 2 A48406 annexin VI homolog
39 19 26.4 20 2 S50203 zona pellucida gly
40 18 25.0 10 2 A37268 Ig heavy chain C r
41 18 25.0 12 2 S51737 T-cell receptor be
42 18 25.0 12 2 PH0771 T-cell receptor tw
43 18 25.0 13 2 S01904 H+-transporting tw
44 18 25.0 14 2 PT0254 Ig heavy chain CRD
45 18 25.0 14 2 PH1608 Ig H chain V-D-J r

ALIGNMENTS

RESULT 1

B40741
T-cell receptor beta chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: B40741
R:Mallick, C.A.; Dudley, E.C.; Viney, J.L.; Owen, M.J.; Hayday, A.C.
Cell 73, 513-519, 1993
A:Title: Rearrangement and diversity of T cell receptor beta chain genes in thymocytes:
A:Reference number: A40741; MUID:93258815; PMID:8387894
A:Accession: B40741
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-18 <MAL>
A:Cross-references: GB:S60903; NID:G300356; PIDN:AAB26614.1; PID:G300357
A:Experimental source: thymocytes, clone 1.V5
A:Note: sequence extracted from NCBI backbone (NCBIN:131689, NCBIP:131693)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 33.3%; Score 24; DB 2; Length 18;
Best Local Similarity 23.1%; Pred. No. 5.5e+02;
Matches 3; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 CITQYERESQAY 13
DB 3 CASSRDRDQTQYF 15

RESULT 2

PH1605
Ig H chain V-D-J region (wild-type clone 328) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1605
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 176, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
A:Reference number: PH1580; MUID:93301609; PMID:8315387
A:Accession: PH1605
A:Molecule type: DNA
A:Residues: 1-12 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 31.9%; Score 23; DB 2; Length 12;
Best Local Similarity 25.0%; Pred. No. 5.5e+02;
Matches 3; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 CITQYERESQAY 12
DB 1 CARRYREDAMDY 12

```
RESULT 3
PT0252
IG heavy chain CDR3 region (clone 2-109D) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0252
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0252
A:Molecule type: DNA
A:Residues: 1-14 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 31.9%; Score 23; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 6.5e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 YERESQAYY 13
DB 4 YYDSSGGY 12

RESULT 4
E49039
T-cell receptor beta chain V-D-J-C region (V beta 1, J beta 1.1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: E49039
R:Rosenberg, W.M.; Moss, P.A.; Bell, J.I.
Eur. J. Immunol. 22, 541-549, 1992
A:Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using
A:Reference number: A49039; MUID:92164737; PMID:1311263
A:Accession: E49039
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-14 <ROS>
A>Note: sequence extracted from NCBI backbone (NCBIP:90717)
C:Keywords: T-cell receptor

Query Match 31.9%; Score 23; DB 2; Length 14;
Best Local Similarity 23.1%; Pred. No. 6.5e+02;
Matches 3; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 CITQYERESQAYY 13
DB 1 CASAGEGDETAFF 13

RESULT 5
S47358
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47358
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-AO201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47358
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35682; NID:G527453; PIDN:CAA84751.1; PID:G527454
C:Keywords: T-cell receptor

Query Match 30.6%; Score 22; DB 2; Length 13;
Best Local Similarity 23.1%; Pred. No. 9.3e+02;
Matches 3; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 1 CITQYERESQAYY 13
DB 1 CASSYRNQOPHF 13

RESULT 6
A17340
ribonucleoside-diphosphate reductase (EC 1.17.4.1), adenosylcobalamin-dependent - coryn-
C:Species: coryneform bacterium ATCC11425
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C:Accession: A17340
R:Tsal, P.K.; Hogenkamp, H.P.C.
J. Biol. Chem. 255, 1273-1278, 1980
A:Title: The purification and characterization of an adenosylcobalamin-dependent ribonu-
A:Reference number: A17340; MUID:80115631; PMID:6986368
A>Note: Corynebacterium nephridii
A:Accession: A17340
A:Molecule type: protein
A:Residues: 1-15 <TSA>
A:Cross-references: UNIPROT:Q7MOK8
C:Keywords: oxidoreductase

Query Match 30.6%; Score 22; DB 2; Length 15;
Best Local Similarity 30.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 4 QYERESQAYY 13
DB 6 RFTKENQSAAY 15

RESULT 7
AS3608
neurotensin - guinea pig
C:Species: Cavia porcellus (guinea pig)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: AS3608
R:Shaw, C.; Thim, L.; Conlon, J.M.
FEBS Lett. 202, 187-191, 1986
A:Title: [Ser(7)]neurotensin: isolation from guinea pig intestine.
A:Reference number: AS3608; MUID:86248085; PMID:3087775
A:Accession: AS3608
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <SHA>
A:Cross-references: UNIPROT:P32560
C:Superfamily: neurotensin
C:Keywords: neuropeptide; pyroglutamic acid
F:1/Modified site: pyroglutamic acid (Gln) #status experimental

Query Match 29.2%; Score 21; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 YERESQAYY 13
DB 3 YENKSRPPY 11

RESULT 8
CA0944
hypothetical protein (1-phosphofructokinase 5' region) - Xanthomonas campestris pv. cam-
C:Species: Xanthomonas campestris pv. campestris
C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C:Accession: CA0944
R:de Crecy-Lagard, V.; Bouvet, O.M.M.; Lejeune, P.; Danchin, A.
J. Biol. Chem. 266, 18154-18161, 1991
A:Title: Fructose catabolism in Xanthomonas campestris pv. campestris. Sequence of the
A:Reference number: A40944; MUID:92011547; PMID:1655739
A:Accession: CA0944
A:Molecule type: DNA
A:Residues: 1-14 <DE3>
```

A;Cross-references: UNIPROT:P45597; GB:M69242; NID:gl155366; PIDN:AAA27600.1; PID:gl155367
 C;Superfamily: fructose phosphotransferase multiphosphoryltransfer protein; phosphotransferase system phosphohistidine-containing protein homology

Query Match 29.2%; Score 21; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 1.5e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 ERESQA 11
 :|||
 Db 9 QREGQA 14

RESULT 9
 B44036 collagen alpha 1(XII) chain NC3B domain - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: B44036
 R;Lunstrum, G.P.; McDonough, A.M.; Marinkovich, M.P.; Keene, D.R.; Morris, N.P.; Burgess
 J. Biol. Chem. 267, 20087-20092, 1992
 A;Title: Identification and partial purification of a large, variant form of type XII co
 A;Reference number: A44036; MUID:93015874; PMID:1400326
 A;Accession: B44036
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-16 <LUN>
 A;Cross-references: UNIPROT:Q9TRM5
 A;Experimental source: skin
 A;Note: sequence extracted from NCBI backbone (NCBIP:115796)

Query Match 29.2%; Score 21; DB 2; Length 16;
 Best Local Similarity 37.5%; Pred. No. 1.8e+03;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CITQYERE 8
 :|||
 Db 3 CLTRAED 10

RESULT 10
 PX0059 trypsin inhibitor chain A - Acacia confusa (fragment)
 C;Species: Acacia confusa
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 17-Mar-2000
 C;Accession: PX0059
 R;Lin, J.; Chu, S.; Wu, H.; Hsieh, Y.
 J. Biochem. 110, 879-883, 1991
 A;Title: Trypsin inhibitor from the seeds of Acacia confusa.
 A;Reference number: PX0059; MUID:92176160; PMID:1794977
 A;Accession: PX0059
 A;Molecule type: protein
 A;Residues: 1-20 <LIN>
 C;Superfamily: plant Kunitz-type proteinase inhibitor
 C;Keywords: serine proteinase inhibitor

Query Match 29.2%; Score 21; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 2.2e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 RESQAYY 13
 :|||
 Db 12 RNGGAYY 18

RESULT 11
 A47105 dystroglycan - chicken (fragment)
 N;Alternate names: laminin-binding protein 120
 C;Species: Gallus gallus (chicken)
 C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A47105
 R;Gee, S.H.; Blacher, R.W.; Douville, P.J.; Provost, P.R.; Yurchenco, P.D.; Carbonetto,

J. Biol. Chem. 268, 14972-14980, 1993
 A;Title: Laminin-binding protein 120 from brain is closely related to the dystrophin-as
 photransferase system phosphohistidine-containing protein homology
 A;Reference number: A47105; MUID:93315474; PMID:8325873
 A;Accession: A47105
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-20 <GEE>
 A;Cross-references: UNIPROT:Q9PRM4
 A;Experimental source: embryonic brain
 A;Note: sequence extracted from NCBI backbone (NCBIP:134982)
 C;Keywords: heparin binding

Query Match 29.2%; Score 21; DB 2; Length 20;
 Best Local Similarity 40.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 QYERESQAYY 13
 :|||
 Db 3 QFNNSQLMY 12

RESULT 12
 A39703 tubulin beta-3 chain - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 09-Jul-2004
 C;Accession: A39703
 R;Alexander, J.E.; Hunt, D.F.; Lee, M.K.; Shabanowitz, J.; Michel, H.; Berlin, S.C.; Ma
 Proc. Natl. Acad. Sci. U.S.A. 88, 4685-4689, 1991
 A;Title: Characterization of posttranslational modifications in neuron-specific class I
 A;Reference number: A39703; MUID:91271258; PMID:2052551
 A;Accession: A39703
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-14 <ALL>
 A;Cross-references: UNIPROT:Q7M2L3

Query Match 27.8%; Score 20; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 2.4e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 ERESQA 11
 :|||
 Db 5 ERESEA 10

RESULT 13
 PHI613 Ig H chain V-D-J region (clone B-less 17) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C;Accession: PHI613
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
 A;Reference number: PHI580; MUID:93301609; PMID:8315387
 A;Accession: PHI613
 A;Molecule type: DNA
 A;Residues: 1-15 <LEV>
 A;Experimental source: bone marrow pre-B lymphocyte
 C;Keywords: immunoglobulin

Query Match 27.8%; Score 20; DB 2; Length 15;
 Best Local Similarity 42.9%; Pred. No. 2.5e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 RESQAYY 13
 :|||
 Db 3 RRTMWY 9

RESULT 14

```

GMSH
gastrin - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 20-Mar-1998
C:Accession: A01619
R:Agarwal, K.L.; Beacham, J.; Bentley, P.H.; Gregory, R.A.; Kenner, G.W.; Sheppard, R.C.
Nature 219, 614-615, 1968
A:Title: Isolation, structure and synthesis of ovine and bovine gastrins.
A:Reference number: A01619; MUID:68357500; PMID:5665711
A:Accession: A01619
A:Molecule type: protein
A:Residues: 1-17 <AGA>
C:Superfamily: gastrin
F:1/Modified site: amidated carboxyl end; hormone; pancreas; phosphoprotein; pyroglutamic acid;
F:12/Binding site: pyroglutamate carboxylic acid (Gln) #status experimental
F:17/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 27.8%; Score 20; DB 1; Length 17;
Best Local Similarity 57.1%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ERESQAY 12
DB 6 EEEEAAY 12

RESULT 15
A60071
gastrin - rhesus macaque
C:Species: Macaca mulatta (rhesus macaque)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C:Accession: A60071
R:Yu, J.; Xin, Y.; Eng, J.; Yalow, R.S.
Regul. Pept. 32, 39-45, 1991
A:Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences.
A:Reference number: A60071; MUID:91164506; PMID:2003150
A:Accession: A60071
A:Molecule type: protein
A:Residues: 1-17 <YUA>
A:Cross-references: UNIPROT:P33714
C:Superfamily: gastrin
F:1/Modified site: amidated carboxyl end; hormone; intestine; pyroglutamic acid; sulfoprotein
F:12/Binding site: pyroglutamate carboxylic acid (Gln) #status experimental
F:17/Modified site: sulfatate (Tyr) (covalent) (partial) #status experimental

Query Match 27.8%; Score 20; DB 2; Length 17;
Best Local Similarity 57.1%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ERESQAY 12
DB 6 EEEEAAY 12

Search completed: September 15, 2005, 16:39:56
Job time : 31.5 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2005, 15:50:48 ; Search time 121 Seconds
(without alignments)
41.553 Million cell updates/sec

Title: US-09-576-724-1

Perfect score: 72

Sequence: 1 CITQYRESQAYY 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 716780

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesep16Dec04:*
1: genesep1980s:*
2: genesep1990s:*
3: genesep2000s:*
4: genesep2001s:*
5: genesep2002s:*
6: genesep2003as:*
7: genesep2003bs:*
8: genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	13	5	Abb08378 Mutant im
2	72	100.0	13	7	Add24246 Human pri
3	72	100.0	15	7	Adc53154 Immunolog
4	72	100.0	18	5	Abb80955 Prion E3
5	69	95.8	13	5	Abb08379 Immunogen
6	69	95.8	13	7	Add24247 Bovine pr
7	69	95.8	13	7	Adf65802 Prion pro
8	69	95.8	15	2	Aar38048 Prion pro
9	69	95.8	17	4	Aab69083 Bovine pr
10	69	95.8	19	5	Abb81632 Prion mim
11	69	95.8	19	7	Abu64310 Transmiss
12	69	95.8	19	8	Ado04597 Prion mim
13	65	90.3	20	7	Add24243 Mouse pri
14	60	83.3	12	8	Adl15228 Bovine pr
15	60	83.3	12	8	Adl15244 Bovine pr
16	56	77.8	11	8	Adl15241 Bovine pr
17	56	77.8	14	8	Adl15249 Bovine pr
18	56	77.8	15	8	Adl15264 Bovine pr
19	46	63.9	19	8	Adl15217 Bovine pr
20	40	55.6	12	4	Aau25361 Schizophr
21	40	55.6	12	4	Aau15705 Schizophr
22	40	55.6	12	6	Abp55138 Human pri
23	40	55.6	12	6	Ado78972 Schizophr
24	37	51.4	11	3	Aab15060 Human pri
25	37	51.4	12	2	Aaw35546 Immunizat

26	37	51.4	12	3	AAB15065	Aab15065 Sheep pri
27	37	51.4	12	3	RAB15064	Aab15064 Cattle pr
28	37	51.4	12	6	ABP55131	Abp55131 Bovine pr
29	37	51.4	12	8	ADL15218	Adl15218 Bovine pr
30	37	51.4	12	8	ADL15236	Adl15236 Bovine pr
31	37	51.4	15	8	ADL15261	Adl15261 Bovine pr
32	34	47.2	12	3	RAB15063	Aab15063 Mouse pri
33	34	47.2	12	3	RAB15062	Aab15062 Hamster p
34	34	47.2	16	2	AAS54046	Aaw54046 C. parvum
35	32	44.4	8	6	ABP55135	Abp55135 Prion pro
36	32	44.4	14	2	AAR89153	Aar89153 CAEV env
37	31	43.1	20	4	AAB66615	Aab66615 Mouse pri
38	30	41.7	12	2	AAR37250	Aar37250 IL-6 anta
39	30	41.7	13	8	ADL15216	Adl15216 Bovine pr
40	29	40.3	17	2	AA118295	Aay18295 Tendami
41	29	40.3	17	3	AA166905	Aay66905 T cell an
42	29	40.3	18	5	ABG96643	Abg96643 Human leu
43	29	40.3	20	4	AAU02715	Aau02715 CDR regio
44	29	40.3	20	8	ADH15361	Adh15361 Gliadin r
45	29	40.3	20	8	ADH16090	Adh16090 Gliadin r

ALIGNMENTS

RESULT 1
ABB08378 ID ABB08378 standard; peptide; 13 AA.
XX AC ABB08378;
XX DT 22-APR-2002 (first entry)
XX DE Mutant immunogenic peptide derived from bovine prion protein.
XX KW Prion; BSE; bovine spongiform encephalopathy; vCJD;
KW new variant creutzfeldt jacobs disease; scrapie; TSE;
KW transmissible spongiform encephalopathy; antibody; PrPSc; PrPC; vaccine;
KW CJD; creutzfeldt jacobs disease; cow.
XX OS Bos taurus.
XX FH Key Location/Qualifiers
FT Misc-difference 6 /note= "wild-type Gln is replaced by Glu."
XX PN EP1158003-A1.
XX PD 28-NOV-2001.
XX PF 23-MAY-2000; 2000EP-00111108.
XX PR 23-MAY-2000; 2000EP-00111108.
XX PA (BLOO-) BLOOD TRANSFUSION CENT SLOVENIA.
XX PI Curin-Serbec;
XX WPI; 2002-107827/15.
XX PT New antibody, useful in diagnosis and treatment of BSE, CJD, new variant
PT CJD and other Transmissible Spongiform Encephalopathy related diseases,
XX selectively binds to the infectious form of the prion protein.
XX Claim 3; Page 10; 21pp; English.
XX The invention relates to an antibody selectively binding to the three
CC dimensional conformation of the C-terminal of the infectious 'scrapie',
CC (PrPSc) isoform of the prion protein (or a part), but not binding to the
CC structure of the C-terminal of the normal cellular (PrPc) isoform of the
CC prion protein. The antibodies (or functional parts) are useful in the
CC diagnosis of Bovine Spongiform Encephalopathy (BSE), Creutzfeldt Jacobs
CC Disease (CJD), new variant form CJD (vCJD) and other Transmissible

CC Spongiform Encephalopathy (TSE) related diseases e.g. in humans, cows,
 CC sheep etc., since they can differentiate between the infectious (PrPSc)
 CC isoform and the normal cellular (PrPc) isoform of the prion protein. They
 CC are also useful in the treatment of such diseases. They may be included in
 CC pharmaceutical compositions or used to produce drugs or active and/or
 CC passive vaccines against diseases as above. The anti-idiotypic antibodies
 CC of the polypeptides of the invention may also be used to produce drugs or
 CC vaccines against such diseases. The current sequence represents a mutant
 CC immunogenic peptide derived from bovine prion protein C-terminal region
 CC (see ABB08377). This sequence is created from the wild-type sequence by
 CC replacement of the Gln residue at position 6 of the peptide with Glu.
 CC This sequence has proven to elicit an immune response sufficiently strong
 CC enough to be capable of easily raising antibodies specifically against
 CC PrPSc

XX SQ Sequence 13 AA;
 Query Match 100.0%; Score 72; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.9e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CITQYERESQAYY 13
 Db 1 CITQYERESQAYY 13
 |||||

RESULT 2
 ADD24246
 ID ADD24246 standard; peptide; 13 AA.

XX AC ADD24246;

XX DT 15-JAN-2004 (first entry)

XX DE Human prion protein PrP peptide 214-226.

XX KW vaccine composition; virus-like particle; core particle;
 KW first attachment site; antigen; antigenic determinant; prion protein;
 KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
 KW prion disease; Bovine Spongiform Encephalopathy; BSE;
 KW Creutzfeldt-Jakob Disease; prion.

XX OS prion.

XX FN WO2003059386-A2.

XX PD 24-JUL-2003.

XX PF 17-JAN-2003; 2003WO-EP000460.

XX PR 18-JAN-2002; 2002US-00050902.

XX PR 21-JAN-2002; 2002WO-IB000166.

XX PR 08-JUL-2002; 2002US-0393725P.

XX PR 18-JUL-2002; 2002US-0396590P.

XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX PI Bachmann M, Maurer P, Pelliccioli E, Renner WA;

XX DR WPI; 2003-598483/56.

XX A vaccine composition for preventing or treating prion diseases (e.g.
 XX Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-
 XX phage) and at least one prion protein or peptide bound to the virus-like
 XX particle.

XX FS Disclosure; Page 86; 246pp; English.

XX This invention relates to a novel vaccine composition comprising a virus-
 CC like or a core particle with at least one first attachment site and at
 CC least one antigen or antigenic determinant that is a prion protein (PrP)
 CC or its dimer, or a PrP peptide, the antigen or antigenic determinant
 CC being bound to the virus-like or core particle. The vaccine of the

CC invention may have neuroprotective or antiinflammatory activity. The
 CC composition is useful as a medicament or in manufacturing a medicament
 CC for the treatment or prevention of prion diseases. The prion diseases may
 CC include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
 CC Disease. The present sequence is that of a peptide fragment of a prion
 CC protein which may be used for the production of the vaccine of the
 CC invention.

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 72; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.9e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CITQYERESQAYY 13
 Db 1 CITQYERESQAYY 13
 |||||

RESULT 3
 ADC53154

ID ADC53154 standard; peptide; 15 AA.

XX AC ADC53154;

XX DT 18-DEC-2003 (first entry)

XX DE Immunological assay related Igg peptide 2.

XX KW analogue; immunoassay; coupled; antigenic; toxic; infectious;
 KW immunological; Igg.

XX OS Unidentified.

XX PN JP2003111592-A.

XX PD 15-APR-2003.

XX PF 04-OCT-2001; 2001JP-00308464.

XX PR 04-OCT-2001; 2001JP-00308464.

XX PA (MENE-) MENEKI SEIBUTSU KENKYUSHO KK.

XX DR WPI; 2003-601766/57.

XX PT Novel analog of a test substance to be measured by immunoassay, has
 PT peptide with two antigenic determinants similar to the antigenic
 PT determinants of test substance, coupled to both ends of basic peptide
 PT sequence.

XX PS Example 3; SEQ ID NO 8; 10pp; Japanese.

XX CC The invention relates to a novel immunological analogue of a test
 CC substance to be measured by an immunoassay, which contains a peptide
 CC sequence coupled to both ends of a basic peptide sequence. The peptide
 CC sequence comprises two different antigenic determinants which are similar
 CC to the antigenic determinants present in the test substance. The
 CC immunoassay has the advantage of toxic and infectious proteins being
 CC determined safely and simply. This sequence represents an Igg peptide
 CC used in the method of the invention.

XX SQ Sequence 15 AA;

Query Match 100.0%; Score 72; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CITQYERESQAYY 13
 Db 1 CITQYERESQAYY 13
 |||||

XX	EF1158003-A1.
PN	XX
XX	XX
PD	28-NOV-2001.
XX	XX
PF	23-MAY-2000; 2000EP-00111108.
PP	XX
PR	23-MAY-2000; 2000EP-00111108.
XX	(BLOO-) BLOOD TRANSFUSION CENT SLOVENIA.
XX	XX
PI	Curin-Serbec;
XX	XX
DR	WPI; 2002-107827/15.
XX	XX
PT	New antibody, useful in diagnosis and treatment of BSE, CJD, new variant
PT	CJD and other Transmissible Spongiform Encephalopathy related diseases,
PT	selectively binds to the infectious form of the prion protein.
XX	XX
PS	Claim 18; Page 11; 21pp; English.
XX	XX
CC	The invention relates to an antibody selectively binding to the three
CC	dimensional conformation of the C-terminal of the infectious 'scrapie'
CC	(PrPSc) isoform of the prion protein (or a part), but not binding to the
CC	structure of the C-terminal of the normal cellular (PrPc) isoform of the
CC	prion protein. The antibodies (or functional parts) are useful in the
CC	diagnosis of Bovine Spongiform Encephalopathy (BSE), Creutzfeldt Jacobs
CC	Disease (CJD), new variant form CJD (vCJD) and other Transmissible
CC	Spongiform Encephalopathy (TSE) related diseases e.g. in humans, cows,
CC	sheep etc., since they can differentiate between the infectious (PrPSc)
CC	isoform and the normal cellular (PrPc) isoform of the prion protein. They
CC	are also useful in the treatment of such diseases.They may be included in
CC	pharmaceutical compositions or used to produce drugs or active and/or
CC	passive vaccines against diseases as above. The antidiotypic antibodies
CC	of the polypeptides of the invention may also be used to produce drugs or
CC	vaccines against such diseases. The current sequence represents an
CC	immunogenic peptide derived from bovine prion protein C-terminal region
CC	(see ABB08377)
XX	XX
SQ	Sequence 13 AA;
Query Match 95.8%; Score 69; DB 5; Length 13;	
Best Local Similarity 92.3%; Pred. NO. 1e-05;	
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 CITQVERSOAAY 13
Db	1 CITQVERSOAAY 13
RESULT 6	
ADD24247	
ID	ADD24247 standard; peptide; 13 AA.
XX	XX
AC	ADD24247;
XX	XX
DT	15-JAN-2004 (first entry)
DE	Bovine prion protein PrP peptide 225-237.
XX	XX
KW	vaccine composition; virus-like particle; core particle;
KW	first attachment site; antigen; antigenic determinant; prion protein;
KW	PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
KW	prion disease; Bovine Spongiform Encephalopathy; BSE;
KW	Creutzfeldt-Jakob Disease; prion.
XX	XX
OS	prion.
XX	XX
WO	WO2003059386-A2.
PN	XX
XX	XX
PD	24-JUL-2003.
XX	XX
PF	17-JAN-2003; 2003WO-EP000460.

PS Claim 29; Page 74; 82pp; English.

XX The sequences given in AAR38041-48 represent polypeptides which are

CC derived from an antigenic site, region F, of a prion protein. Prion

CC proteins comprise six regions of interest (A-F), and two related frame

CC shift peptides sequences caused by a repeating section in region E having

CC a nucleic acid coding sequence frame shift mutation of +1 (PSa) or -1

CC (FSb). These peptides (see also AAR38041-48) and antibodies raised

CC against these may be used to treat or prevent spongiform encephalopathy

CC in humans, sheep or cattle. They can be used to block cellular binding

CC and aggregation of prion proteins and to stimulate the mammalian immune

CC system. These peptides may be used to distinguish between the normal form

CC of prion protein (PrP^C) and the scrapie-associated form (PrP^{Sc}). These

CC peptides may include rare or synthetic amino acids or a ratio- inverse

CC peptide modification to improve resistance to enzymatic degradation.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 15 AA;

SQ

Query Match 95.8%; Score 69; DB 2; Length 15;

Best Local Similarity 92.3%; Pred. No. 1.2e-05;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQVERESQAYY 13

DB |||||:|||||

1 CITQVERESQAYY 13

RESULT 9

AAB69083

ID AAB69083 standard; peptide; 17 AA.

XX AAB69083;

AC

XX 23-APR-2001 (first entry)

DT

XX Bovine prion protein peptide SEQ ID NO:3.

XX

DE Monoclonal antibody; detection; prion protein; TSE; infection;

XX transmissible spongiform encephalopathy; scrapie; bovine encephalopathy;

KW chronic wasting disease; PrP-Sc.

KW

XX Bos taurus.

XX

OS WO200105426-A1.

PN

XX 25-JAN-2001.

PD

XX 14-JUL-2000; 2000WO-US019211.

PF

XX 15-JUL-1999; 99US-00353348.

PR

XX (USDA) US DEPT OF AGRICULTURE.

PA

XX O'rourke KI;

PI

XX WPI; 2001-159477/16.

DR

XX Monoclonal antibodies for detecting prior proteins as an indication of

PT transmissible spongiform encephalopathies, specifically binds to

PT conserved group of prior proteins.

PS

XX Example 2; Page 12; 25pp; English.

XX

CC The present invention describes a monoclonal antibody (I) which

CC specifically binds to a conserved epitope of prion proteins, which is

CC capable of binding prion protein (PrP)-Sc protein in fixed or unfixed

CC tissue that has been treated to unmask the group to PrP-Sc protein and

CC eliminate availability of a corresponding group of PrP-Cellular. (I) can

CC be used in immunoassays to detect PrP-Sc proteins in animal or human,

CC including ruminant livestock, cats, mink and non-human primates, sheep,

CC goat, cattle, mule deer and elk, as an indication of the presence of

CC transmissible spongiform encephalopathies (TSE). Presence of PrP-Sc

CC

CC indicates the scrapie-, bovine encephalopathy- or chronic wasting disease

CC infected animals. The antibodies provide early detection of PrP-Sc and

CC for preclinical diagnosis of TSE. The present sequence represents a prion

CC protein peptide which is used in an example from the present invention

XX

SQ Sequence 17 AA;

Query Match 95.8%; Score 69; DB 4; Length 17;

Best Local Similarity 92.3%; Pred. No. 1.4e-05;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CITQVERESQAYY 13

DB |||||:|||||

1 CITQVERESQAYY 13

RESULT 10

ABB81632

ID ABB81632 standard; peptide; 19 AA.

XX

AC ABB81632;

XX

DT 25-SEP-2002 (first entry)

DT

XX Prion mimetic peptide SEQ ID NO:4.

XX

DE Prion mimetic peptide; degradation; detection; TSE; infection;

KW transmissible spongiform encephalopathy; prion protein; sterilisation;

KW immunisation; Creutzfeldt-Jacob disease; kuru; fatal familial insomnia;

KW Gerstmann-Strausler-Scheinker syndrome; chronic wasting disease;

KW bovine spongiform encephalopathy; feline spongiform encephalopathy;

KW scrapie; transmissible mink encephalopathy.

XX

OS Synthetic.

OS

XX WO200253723-A2.

PN

XX 11-JUL-2002.

PD

XX 08-JAN-2002; 2002WO-GB0000052.

PF

XX 08-JAN-2001; 2001GB-00000420.

PR

XX 26-FEB-2001; 2001GB-00004696.

PR

XX (MICR-) MICROBIOLOGICAL RES AUTHORITY.

PA

XX Raven NDH;

PI

XX WPI; 2002-557743/59.

DR

XX Inactivating transmissible spongiform encephalopathy (TSE) agent such as

PT Creutzfeldt-Jacob disease, scrapie, kuru or Gerstmann-Strausler-

PT Scheinker syndrome involves exposing agent to thermostable proteolytic

PT enzyme.

XX

XX Example; Page 19; 41pp; English.

XX

CC The present invention describes a method (M1) for inactivating a

CC transmissible spongiform encephalopathy (TSE) agent comprising exposing

CC the TSE agent to a thermostable proteolytic enzyme. Also described: (1) a

CC composition (I) for inactivating a TSE agent, comprising a thermostable

CC proteolytic enzyme; (2) an antibody (II) specific for a prion dimer which

CC does not bind to a prion monomer; and (3) a purified prion dimer. (M1) is

CC useful for inactivating a TSE agent such as a prion. A TSE agent is

CC Creutzfeldt-Jacob disease or its variant, kuru, fatal familial insomnia,

CC Gerstmann-Strausler-Scheinker syndrome, bovine spongiform

CC encephalopathy, scrapie, feline spongiform encephalopathy, chronic

CC wasting disease or transmissible mink encephalopathy. (I) is useful for

CC sterilising material contaminated with the TSE agent. A prion dimer is

CC useful for examining a sample infected with or suspected to be infected

CC by a prion protein, and for detecting prion infectivity, by detecting a

CC prion dimer in the sample. A prion dimer is useful for producing (II), by

CC immunising an animal with a prion dimer, obtaining its extract which

CC contains (II), and isolating (II) from the extract. The method comprises
 CC obtaining an antibody preparation containing antibodies which bind a
 CC prion dimer, and removing (II) from the preparation. (MI) and (I) are
 CC useful for inactivating TSE agents in potentially contaminated clinical
 CC waste and culled animal material. (MI) is useful for sterilising larger
 CC surface areas of apparatus, operating tables or even walls of rooms. The
 CC present sequence represents a prion mimetic peptide which is used in an
 CC example from the present invention in the preparation of antibodies
 CC including dimer preferential antibodies

XX SQ Sequence 19 AA;

Query Match 95.8%; Score 69; DB 5; Length 19;

Best Local Similarity 92.3%; Pred. No. 1.6e-05;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CITQYERESQAYY 13
 |||||:|||||
 Db 1 CITQYERESQAYY 13

RESULT 11

ID ABU64310 standard; peptide; 19 AA.

XX AC ABU64310;

XX DT 11-MAR-2004 (first entry)

XX DE Transmissible spongiform encephalopathy prion protein fragment #8.

XX KW Transmissible spongiform encephalopathy; TSE; antibody; dimer;

XX KW antiinflammatory; neuroprotective; sedative.

XX OS Unidentified.

XX FN WO2003080665-A2.

XX PD 02-OCT-2003.

XX PF 20-MAR-2003; 2003WO-GB001295.

XX PR 20-MAR-2002; 2002GB-00006594.

XX PR 11-JUL-2002; 2002GB-00016098.

XX PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.

XX PI Raven NDH, Sutton JM, Murdoch H;

XX DR WPI; 2003-779246/73.

XX PT Treating transmissible spongiform encephalopathy (TSE) infection
 XX PT comprises administering an antibody that binds to a dimer of a prion
 XX PT protein.

XX PS Claim 5; Page 40; 40pp; English.

XX CC The present invention relates to a method of treating transmissible
 XX CC spongiform encephalopathy (TSE) infection, comprising administering an
 XX CC antibody that binds to a dimer of a prion protein. The methods and
 XX CC compositions are useful for treating TSE, Creutzfeld-Jacob disease,
 XX CC variant Creutzfeld-Jacob disease, Kuru, fatal familial insomnia,
 XX CC Gerstmann-Strausler-Scheinker syndrome, bovine spongiform
 XX CC encephalopathy, scrapie, feline spongiform encephalopathy, chronic
 XX CC wasting disease and transmissible mink encephalopathy. Antigens are
 XX CC useful for the manufacture of a medicament for stimulating antibody
 XX CC production. The present sequence is a peptide fragment of a TSE prion
 XX CC protein

XX SQ Sequence 19 AA;

Query Match 95.8%; Score 69; DB 7; Length 19;

Best Local Similarity 92.3%; Pred. No. 1.6e-05;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CITQYERESQAYY 13
 |||||:|||||
 Db 1 CITQYERESQAYY 13

RESULT 12

ID ADO04597 standard; peptide; 19 AA.

XX AC ADO04597;

XX DT 29-JUL-2004 (first entry)

XX DE Prion mimetic peptide, 6.

XX KW Transmissible spongiform encephalopathy; TSE; Creutzfeld-Jacob disease;
 XX KW Kuru; fatal familial insomnia; Gerstmann-Strausler-Scheinker syndrome;
 XX KW bovine spongiform encephalopathy; BSE; scrapie;
 XX KW feline spongiform encephalopathy; chronic wasting disease;
 XX KW transmissible mink encephalopathy; sterilisation; prion.

XX OS Unidentified.

XX FN US2004091474-A1.

XX PD 13-MAY-2004.

XX PF 08-JUL-2003; 2003US-00614370.

XX PR 08-JAN-2001; 2001GB-00000420.

XX PR 26-FEB-2001; 2001GB-00004696.

XX PR 08-JAN-2002; 2002WO-GB000052.

XX PR 11-JUL-2002; 2002GB-00016146.

XX PA (HEAL-) HEALTH PROTECTION AGENCY.

XX PI Raven NDH, Sutton JM;

XX DR WPI; 2004-374912/35.

XX PT Inactivating transmissible spongiform encephalopathy (TSE) agent, PT
 XX PT involves exposing TSE agent to thermostable proteolytic enzyme such as
 XX PT subtilisin.

XX PS Example 1; SEQ ID NO 4; 49pp; English.

XX CC The invention relates to a method of inactivating a transmissible
 XX CC spongiform encephalopathy (TSE) agent. The method involves exposing the
 XX CC TSE agent to a thermostable proteolytic enzyme such as subtilisin. The
 XX CC invention is useful for inactivating a transmissible spongiform
 XX CC encephalopathy (TSE) agent selected from Creutzfeld-Jacob disease,
 XX CC variant Creutzfeld-Jacob disease, Kuru, fatal familial insomnia,
 XX CC Gerstmann-Strausler-Scheinker syndrome, bovine spongiform encephalopathy
 XX CC (BSE), scrapie, feline spongiform encephalopathy, chronic wasting disease
 XX CC and transmissible mink encephalopathy. The invention is useful for
 XX CC sterilising medical apparatus and for inactivation of TSE agents in
 XX CC potentially contaminated clinical waste and culled animal material. The
 XX CC present sequence is a prion mimetic peptide. This sequence is used to
 XX CC illustrate the method of the invention.

XX SQ Sequence 19 AA;

Query Match 95.8%; Score 69; DB 8; Length 19;

Best Local Similarity 92.3%; Pred. No. 1.6e-05;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CITQYERESQAYY 13
 |||||:|||||
 Db 1 CITQYERESQAYY 13

```

RESULT 13
ADD24243
ID ADD24243 standard; peptide; 20 AA.
XX
AC ADD24243;
XX
DT 15-JAN-2004 (first entry)
XX
DE Mouse prion protein PrP peptide #2.
XX
XX vaccine composition; virus-like particle; core particle;
KW first attachment site; antigen; antigenic determinant; prion protein;
KW PrP; PrP peptide; vaccine; neuroprotective; antiinflammatory;
KW prion disease; Bovine Spongiform Encephalopathy; BSE;
KW Creutzfeldt-Jakob Disease; prion.
XX
OS prion.
XX
XX WO2003059386-A2.
XX
XX 24-JUL-2003.
XX
XX 17-JAN-2003; 2003WO-EP000460.
XX
XX 18-JAN-2002; 2002US-00050902.
XX
XX 21-JAN-2002; 2002WO-IB000166.
XX
XX 08-JUL-2002; 2002US-0393725P.
XX
XX 18-JUL-2002; 2002US-0396590P.
XX
XX (CVTO-) CYTOS BIOTECHNOLOGY AG.
XX
XX Bachmann M, Maurer P, Pelliccioli E, Renner WA;
XX
XX WPI; 2003-598483/56.
XX
XX A vaccine composition for preventing or treating prion diseases (e.g.
XX Creutzfeldt-Jakob Disease) comprises a virus-like particle (e.g. RNA-
XX phase) and at least one prion protein or peptide bound to the virus-like
XX particle.
XX
XX Disclosure; Page 83; 246pp; English.
XX
XX This invention relates to a novel vaccine composition comprising a virus-
XX like or a core particle with at least one first attachment site and at
XX least one antigen or antigenic determinant that is a prion protein (PrP)
XX or its dimer, or a PrP peptide, the antigen or antigenic determinant
XX being bound to the virus-like or core particle. The vaccine of the
XX invention may have neuroprotective or antiinflammatory activity. The
XX composition is useful as a medicament or in manufacturing a medicament
XX for the treatment or prevention of prion diseases. The prion diseases may
XX include Bovine Spongiform Encephalopathy (BSE) or Creutzfeldt-Jakob
XX Disease. The present sequence is that of a peptide fragment of a prion
XX protein which may be used for the production of the vaccine of the
XX invention.
XX
XX Sequence 20 AA;
XX
XX Query Match 90.3%; Score 65; DB 7; Length 20;
XX Best Local Similarity 76.9%; Pred. No. 9.1e-05;
XX Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CITQVERSQAYY 13
XX |:|:|:|:|:|
XX Db 3 CVTQYKESQAYY 15
XX
XX
XX RESULT 14
XX ADL15228
XX ID ADL15228 standard; peptide; 12 AA.
XX
XX AC ADL15228;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX prion; PrPSc; vaccine; Creutzfeldt-Jakob disease; kuru;
XX Gerstmann-Straussler-Sheinker syndrome; fatal familial insomnia;
XX
XX Bovine prion protein PrP peptide - SEQ ID 39.
XX
XX ADL15244 standard; peptide; 12 AA.
XX
XX AC ADL15244;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Bovine prion protein PrP peptide - SEQ ID 39.
XX
XX KW prion; PrPSc; vaccine; Creutzfeldt-Jakob disease; kuru;
XX Gerstmann-Straussler-Sheinker syndrome; fatal familial insomnia;
XX
XX Bovine prion protein PrP peptide - SEQ ID 23.
XX
XX prion; PrPSc; vaccine; Creutzfeldt-Jakob disease; kuru;
XX Gerstmann-Straussler-Sheinker syndrome; fatal familial insomnia;
XX transmissible spongiform encephalopathy;
XX bovine spongiform encephalopathy; BSE; cattle; scrapie; sheep;
XX chronic wasting; deer; elk; mink; cat; bovine; cow; PrP.
XX
XX Bos sp.
XX
XX WO2004018511-A2.
XX
XX 04-MAR-2004.
XX
XX 25-AUG-2003; 2003WO-DK000555.
XX
XX 23-AUG-2002; 2002DK-00001245.
XX
XX (COPE-) COPENHAGEN BIOTECH ASSETS APS.
XX
XX Heegaard P, Jakobsen PH;
XX
XX WPI; 2004-226799/21.
XX
XX Conjugate useful for treating transmissible prion disease, e.g., kuru,
XX comprising two or more peptides or its fragments optionally linked to
XX backbone form to non-linear sequences which mimics tertiary structure of
XX stable prion protein.
XX
XX Claim 13; SEQ ID NO 23; 70pp; English.
XX
XX The invention relates to a novel conjugate comprising two or more peptide
XX fragments optionally linked to a backbone where the peptides are
XX spatially positioned relative to each other to form non-linear sequences
XX which mimic the tertiary structure of pathogenic prion protein PrPSc-
XX specific epitopes and have the same or higher degree of conformational
XX sensitivity to PrPSc. The conjugate of the invention demonstrates
XX neuroprotective activity and may be useful for producing antibodies
XX specific for PrPSc for use in medicine, vaccines, high-throughput
XX screening and as direct probes or reporter substances in assays for
XX detection of PrPSc. Furthermore, the conjugate and peptides may be useful
XX for treating and/or preventing Creutzfeldt-Jakob disease, kuru, Gerstmann
XX -Straussler-Sheinker syndrome, fatal familial insomnia and transmissible
XX spongiform encephalopathies, such as bovine spongiform encephalopathy
XX (BSE) in cattle, scrapie in sheep, chronic wasting disease in deer and
XX elk and transmissible encephalopathies in mink, cat and other animals.
XX The current sequence is that of a bovine prion protein PrP peptide of the
XX invention.
XX
XX Sequence 12 AA;
XX
XX Query Match 83.3%; Score 60; DB 8; Length 12;
XX Best Local Similarity 91.7%; Pred. No. 0.00043;
XX Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 2 ITQYRESQAYY 13
XX |:|:|:|:|:|
XX Db 1 ITQYRESQAYY 12
XX
XX
XX RESULT 15
XX ADL15244
XX ID ADL15244 standard; peptide; 12 AA.
XX
XX AC ADL15244;
XX
XX DT 20-MAY-2004 (first entry)
XX
XX DE Bovine prion protein PrP peptide - SEQ ID 39.
XX
XX KW prion; PrPSc; vaccine; Creutzfeldt-Jakob disease; kuru;
XX Gerstmann-Straussler-Sheinker syndrome; fatal familial insomnia;
XX

```

KW transmissible spongiform encephalopathy;
KW bovine spongiform encephalopathy; BSE; cattle; scrapie; sheep;
KW chronic wasting; deer; elk; mink; cat; bovine; cow; PrP.

XX Bos sp.

XX WO2004018511-A2.

XX 04-MAR-2004.

XX 25-AUG-2003; 2003WO-DK000555.

XX 23-AUG-2002; 2002DK-00001245.

XX (COPE-) COPENHAGEN BIOTECH ASSETS APS.

XX Heegaard P, Jakobsen PH;

XX WPI; 2004-226799/21.

XX Conjugate useful for treating transmissible prion disease, e.g., kuru,
PT comprising two or more peptides or its fragments optionally linked to
PT backbone form to non-linear sequences which mimics tertiary structure of
PT stable prion protein.

XX Claim 15; SEQ ID NO 39; 70pp; English.

XX The invention relates to a novel conjugate comprising two or more peptide
CC fragments optionally linked to a backbone where the peptides are
CC spatially positioned relative to each other to form non-linear sequences
CC which mimic the tertiary structure of pathogenic prion protein PrP^{Sc}-
CC specific epitopes and have the same or higher degree of conformational
CC sensitivity to PrP^{Sc}. The conjugate of the invention demonstrates
CC neuroprotective activity and may be useful for producing antibodies
CC specific for PrP^{Sc} for use in medicine, vaccines, high-throughput
CC screening and as direct probes or reporter substances in assays for
CC detection of PrP^{Sc}. Furthermore, the conjugate and peptides may be useful
CC for treating and/or preventing Creutzfeldt-Jakob disease, kuru, Gerstmann
CC -Straussler-Sheinker syndrome, fatal familial insomnia and transmissible
CC spongiform encephalopathies, such as bovine spongiform encephalopathy
CC (BSE) in cattle, scrapie in sheep, chronic wasting disease in deer and
CC elk and transmissible encephalopathies in mink, cat and other animals.
CC The current sequence is that of a bovine prion protein PrP peptide of the
XX invention.

SQ Sequence 12 AA;

Query Match 83.3%; Score 60; DB 8; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.00043;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ITQYERESQAYY 13
Db 1 ITQYERESQAYY 12

Search completed: September 15, 2005, 16:38:53
Job time : 133 secs